

Exhibit

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Welcome to the SIB BLAST Network Service

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NCBI BLAST program reference [PMID:9254694]:  
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

Query: Q9QZM7; 733 AA  
Date run: 2007-11-13 20:35:31 UTC+0100 on blast01.vital-it.ch  
Program: NCBI BLASTP 2.2.16 [Mar-25-2007]  
Database: UniProtKB Homo sapiens  
82,088 sequences; 35,064,127 total letters  
UniProt Knowledgebase Release 12.4 consists of:  
UniProtKB/Swiss-Prot Release 54.4 of 23-Oct-2007: 287050 entries  
UniProtKB/TrEMBL Release 37.4 of 23-Oct-2007: 4988379 entries

## List of potentially matching sequences

Send selected sequences to   ☐ Include query sequence

	Db	AC	Description	Score	E-value
<input type="checkbox"/>	tr	Q5BJG2	_HUMAN Fibroblast growth factor receptor 1 (Fms-related...	1420	0.0
<input type="checkbox"/>	sp_vs	P11362-14	Isoform 15 of P11362 - Homo sapiens (Human) [FGF...	1420	0.0
<input type="checkbox"/>	sp_vs	P11362-3	Isoform 6 of P11362 - Homo sapiens (Human) [FGFR1...	1415	0.0
<input type="checkbox"/>	sp_vs	P11362-4	Isoform 8 of P11362 - Homo sapiens (Human) [FGFR1...	1407	0.0
<input type="checkbox"/>	sp_vs	P11362-7	Isoform 14 of P11362 - Homo sapiens (Human) [FGFR...	1357	0.0
<input type="checkbox"/>	sp	P11362	FGFR1_HUMAN Basic fibroblast growth factor receptor 1 ...	1352	0.0
<input type="checkbox"/>	tr	Q53H63	_HUMAN Fibroblast growth factor receptor 1 isoform 2 va...	1351	0.0
<input type="checkbox"/>	tr	Q59H40	_HUMAN Fibroblast growth factor receptor 1 isoform 1 va...	1344	0.0
<input type="checkbox"/>	sp_vs	P11362-2	Isoform 4 of P11362 - Homo sapiens (Human) [FGFR1...	1344	0.0
<input type="checkbox"/>	sp_vs	P11362-5	Isoform 10 of P11362 - Homo sapiens (Human) [FGFR...	1275	0.0
<input type="checkbox"/>	sp_vs	P11362-6	Isoform 12 of P11362 - Homo sapiens (Human) [FGFR...	1266	0.0
<input type="checkbox"/>	sp_vs	P21802-3	Isoform 3 of P21802 - Homo sapiens (Human) [FGFR2...	1108	0.0
<input type="checkbox"/>	sp_vs	P21802-18	Isoform 18 of P21802 - Homo sapiens (Human) [FGF...	1100	0.0
<input type="checkbox"/>	sp	P21802	FGFR2_HUMAN Fibroblast growth factor receptor 2 precu...	1065	0.0
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<input type="checkbox"/>	tr	Q1KHY5	_HUMAN Fibroblast growth factor receptor 2 (Bacteria-ex...	1011	0.0
<input type="checkbox"/>	sp_vs	P21802-6	Isoform 6 of P21802 - Homo sapiens (Human) [FGFR2...	1011	0.0
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<input type="checkbox"/>	tr	Q8NI15	_HUMAN Fibroblast growth factor receptor 3 (Fragment) [...	931	0.0
<input type="checkbox"/>	tr	Q8NI16	_HUMAN Fibroblast growth factor receptor 3 (Fragment) [...	929	0.0
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<input type="checkbox"/>	tr	Q8TDA0	_HUMAN Fibroblast growth factor receptor 4 (Fibroblast ...	839	0.0
<input type="checkbox"/>	tr	Q71TW8	_HUMAN Fibroblast growth factor receptor 4, soluble-for...	805	0.0
<input type="checkbox"/>	tr	Q8IXC7	_HUMAN Isoform of FGFR2 [FGFR2 AT-I] [Homo sapiens (Hum...	770	0.0
<input type="checkbox"/>	tr	Q96KE5	_HUMAN Fibroblast growth factor receptor 4 variant [Hom...	735	0.0
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<input type="checkbox"/>	tr	Q59FL9	_HUMAN Fibroblast growth factor receptor 3 isoform 1 va...	684	0.0
<input type="checkbox"/>	tr	A8E633	_HUMAN Putative uncharacterized protein (Fragment) [Hom...	646	0.0
<input type="checkbox"/>	tr	Q0IJ44	_HUMAN FGFR3 protein (Fragment) [FGFR3] [Homo sapiens (...	646	0.0
<input type="checkbox"/>	sp_vs	P22607-3	Isoform 3 of P22607 - Homo sapiens (Human) [FGFR3...	625	e-178
<input type="checkbox"/>	tr	Q59F30	_HUMAN Fibroblast growth factor receptor 4 variant (Fra...	553	e-157
<input type="checkbox"/>	tr	Q9UD50	_HUMAN Fibroblast growth factor receptor subtype 1 (Pra...	516	e-146
<input type="checkbox"/>	sp_vs	P11362-18	Isoform 18 of P11362 - Homo sapiens (Human) [FGF...	468	e-131
<input type="checkbox"/>	tr	Q53G05	_HUMAN Fibroblast growth factor receptor 1 isoform 6 va...	467	e-131
<input type="checkbox"/>	sp_vs	P11362-16	Isoform 17 of P11362 - Homo sapiens (Human) [FGF...	463	e-130
<input type="checkbox"/>	sp_vs	P21802-19	Isoform 19 of P21802 - Homo sapiens (Human) [FGF...	375	e-103
<input type="checkbox"/>	sp	P35968	VGFR2_HUMAN Vascular endothelial growth factor recepto...	325	2e-88
<input type="checkbox"/>	tr	Q59EB0	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) (...	325	2e-88
<input type="checkbox"/>	tr	A2RRS0	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	325	2e-88
<input type="checkbox"/>	tr	Q2VJ45	_HUMAN HOOK3-RET fusion protein [Homo sapiens (Human)]	323	5e-88
<input type="checkbox"/>	tr	Q9BTB0	_HUMAN Ret proto-oncogene [RET] [Homo sapiens (Human)]	323	6e-88
<input type="checkbox"/>	sp	P07949	RET_HUMAN Proto-oncogene tyrosine-protein kinase recep...	323	8e-88
<input type="checkbox"/>	sp	P17948	VGFR1_HUMAN Vascular endothelial growth factor recepto...	322	1e-87
<input type="checkbox"/>	tr	Q5TAR1	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	322	1e-87
<input type="checkbox"/>	tr	Q9UMQ4	_HUMAN RET tyrosine kinase receptor (Fragment) [RET] [H...	319	1e-86
<input type="checkbox"/>	tr	Q15300	_HUMAN RET tyrosine kinase/cAMP protein kinase A subuni...	318	2e-86
<input type="checkbox"/>	tr	Q15850	_HUMAN Urf-ret protein [urf-ret] [Homo sapiens (Human)]	318	2e-86
<input type="checkbox"/>	sp	P35916	VGFR3_HUMAN Vascular endothelial growth factor recepto...	295	1e-79
<input type="checkbox"/>	tr	Q86W08	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	291	3e-78
<input type="checkbox"/>	tr	Q86W07	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	291	3e-78
<input type="checkbox"/>	tr	Q59GQ9	_HUMAN Fms-related tyrosine kinase 1 (Vascular endothel...	291	3e-78
<input type="checkbox"/>	tr	A3E342	_HUMAN IdVEGFR-1 (N2idVEGFR-1) [FLT1] [Homo sapiens (Hu...	290	8e-78
<input type="checkbox"/>	tr	Q06VW7	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	277	5e-74
<input type="checkbox"/>	sp	P07333	CSF1R_HUMAN Macrophage colony-stimulating factor 1 rec...	276	9e-74
<input type="checkbox"/>	tr	Q6IQ28	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	270	6e-72
<input type="checkbox"/>	sp	P10721	KIT_HUMAN Mast/stem cell growth factor receptor precur...	266	7e-71
<input type="checkbox"/>	tr	Q99662	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	266	7e-71
<input type="checkbox"/>	sp	P35590	TIE1_HUMAN Tyrosine-protein kinase receptor Tie-1 prec...	246	1e-64
<input type="checkbox"/>	tr	Q9HBS4	_HUMAN Putative uncharacterized protein [TIE1] [Homo sa...	246	1e-64
<input type="checkbox"/>	sp	Q02763	TIE2_HUMAN Angiopoietin-1 receptor precursor (EC 2.7.1...	240	7e-63
<input type="checkbox"/>	tr	Q5TCU2	_HUMAN TEK tyrosine kinase, endothelial (Venous malform...	240	7e-63
<input type="checkbox"/>	tr	Q59HG2	_HUMAN TEK tyrosine kinase variant (Fragment) [Homo sap...	240	7e-63
<input type="checkbox"/>	tr	Q8IV34	_HUMAN TEK tyrosine kinase, endothelial (Venous malform...	239	2e-62
<input type="checkbox"/>	sp	P08069	IGF1R_HUMAN Insulin-like growth factor 1 receptor prec...	231	3e-60
<input type="checkbox"/>	sp_vs	Q16288-3	Isoform C of Q16288 - Homo sapiens (Human) [NTRK3...	225	2e-58
<input type="checkbox"/>	sp_vs	Q16288-4	Isoform D of Q16288 - Homo sapiens (Human) [NTRK3...	221	3e-57
<input type="checkbox"/>	sp	P06213	INSR_HUMAN Insulin receptor precursor (EC 2.7.10.1) (I...	218	3e-56
<input type="checkbox"/>	tr	Q59H98	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) (...	218	3e-56
<input type="checkbox"/>	tr	Q17RW0	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	218	3e-56
<input type="checkbox"/>	sp_vs	P06213-2	Isoform Short of P06213 - Homo sapiens (Human) [I...	218	3e-56
<input type="checkbox"/>	sp	O15146	MUSK_HUMAN Muscle, skeletal receptor tyrosine protein ...	218	4e-56
<input type="checkbox"/>	tr	Q5VZW8	_HUMAN Muscle, skeletal, receptor tyrosine kinase [MUSK...	218	4e-56
<input type="checkbox"/>	tr	Q5VZW7	_HUMAN Muscle, skeletal, receptor tyrosine kinase [MUSK...	218	4e-56
<input type="checkbox"/>	tr	Q32MJ9	_HUMAN MUSK protein [MUSK] [Homo sapiens (Human)]	218	4e-56
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<input type="checkbox"/>	sp	Q16288	NTRK3_HUMAN NT-3 growth factor receptor precursor (EC ...	216	1e-55
<input type="checkbox"/>	sp	P14616	INSRR_HUMAN Insulin receptor-related protein precursor...	213	9e-55
<input type="checkbox"/>	tr	Q5VZS3	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	213	9e-55

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<input type="checkbox"/>	tr	Q61Q54	_HUMAN PTK7 protein tyrosine kinase 7 [PTK7] [Homo sapi...	211	5e-54
<input type="checkbox"/>	tr	Q5T650	_HUMAN PTK7 protein tyrosine kinase 7 (PTK7 protein tyr...	211	5e-54
<input type="checkbox"/>	sp	P08922	ROS_HUMAN Proto-oncogene tyrosine-protein kinase ROS p...	210	8e-54
<input type="checkbox"/>	tr	Q5TDB4	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	210	8e-54
<input type="checkbox"/>	sp	P04629	NTRK1_HUMAN High affinity nerve growth factor receptor...	209	1e-53
<input type="checkbox"/>	sp	P42679	MARK_HUMAN Megakaryocyte-associated tyrosine-protein k...	209	1e-53
<input type="checkbox"/>	tr	Q9NST8	_HUMAN Putative uncharacterized protein DKFZp434N1212 (...	209	1e-53
<input type="checkbox"/>	tr	A6NF12	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	209	1e-53
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<input type="checkbox"/>	sp	Q16620	NTRK2_HUMAN BDNF/NT-3 growth factors receptor precurs...	209	2e-53
<input type="checkbox"/>	tr	Q5VVP4	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	209	2e-53
<input type="checkbox"/>	tr	Q8NFA8	_HUMAN Transmembrane receptor PTK7-2 (PTK7 protein tyro...	207	7e-53
<input type="checkbox"/>	sp	Q9UM73	ALK_HUMAN ALK tyrosine kinase receptor precursor (EC 2...	206	1e-52
<input type="checkbox"/>	tr	Q8TDJ5	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	206	1e-52
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<input type="checkbox"/>	tr	A6P4T4	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	206	1e-52
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<input type="checkbox"/>	sp	P30530	UFO_HUMAN Tyrosine-protein kinase receptor UFO precurs...	204	3e-52
<input type="checkbox"/>	sp	P42684	ABL2_HUMAN Tyrosine-protein kinase ABL2 (EC 2.7.10.2) ...	204	3e-52
<input type="checkbox"/>	tr	A0M8X0	_HUMAN V-abl Abelson murine leukemia viral oncogene hom...	204	3e-52
<input type="checkbox"/>	sp_vs	P42684-2	Isoform IA of P42684 - Homo sapiens (Human) [ABL2...	204	3e-52
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<input type="checkbox"/>	sp	P16591	FER_HUMAN Proto-oncogene tyrosine-protein kinase FER (...	204	4e-52
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<input type="checkbox"/>	tr	Q8N5L2	_HUMAN AXL receptor tyrosine kinase [AXL] [Homo sapiens...	204	6e-52
<input type="checkbox"/>	sp	P00519	ABL1_HUMAN Proto-oncogene tyrosine-protein kinase ABL1...	203	1e-51
<input type="checkbox"/>	tr	Q59FK4	_HUMAN V-abl Abelson murine leukemia viral oncogene hom...	203	1e-51
<input type="checkbox"/>	tr	Q17R61	_HUMAN V-abl Abelson murine leukemia viral oncogene hom...	203	1e-51
<input type="checkbox"/>	tr	A3KFP3	_HUMAN V-abl Abelson murine leukemia viral oncogene hom...	203	1e-51
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<input type="checkbox"/>	tr	Q1RMG3	_HUMAN MERTK protein [MERTK] [Homo sapiens (Human)]	201	4e-51
<input type="checkbox"/>	sp	Q12866	MERTK_HUMAN Proto-oncogene tyrosine-protein kinase MER...	201	5e-51
<input type="checkbox"/>	sp	P41240	CSK_HUMAN Tyrosine-protein kinase CSK (EC 2.7.10.2) (C...	201	5e-51
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<input type="checkbox"/>	tr	Q16176	_HUMAN Lsk protein [lsk] [Homo sapiens (Human)]	197	5e-50
<input type="checkbox"/>	tr	Q96T36	_HUMAN Fibroblast growth factor receptor 3 IIIC isoform...	196	9e-50
<input type="checkbox"/>	sp	P08631	HCK_HUMAN Tyrosine-protein kinase HCK (EC 2.7.10.2) (p...	195	3e-49
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<input type="checkbox"/>	sp	Q06418	TYRO3_HUMAN Tyrosine-protein kinase receptor TYRO3 pre...	194	3e-49
<input type="checkbox"/>	sp	P06239	LCK_HUMAN Proto-oncogene tyrosine-protein kinase LCK (...	194	3e-49
<input type="checkbox"/>	tr	Q8N6J3	_HUMAN TYRO3 protein (Fragment) [TYRO3] [Homo sapiens (...	194	3e-49
<input type="checkbox"/>	tr	Q7RTZ3	_HUMAN Protein tyrosine kinase (Lymphocyte-specific pro...	194	3e-49
<input type="checkbox"/>	tr	Q59FM9	_HUMAN TYRO3 protein tyrosine kinase variant (Fragment)...	194	3e-49
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<input type="checkbox"/>	tr	Q2VXT0	_HUMAN Proto-oncogene c-fes variant 1 [Homo sapiens (Hu...	193	1e-48
<input type="checkbox"/>	tr	Q2VXS8	_HUMAN Proto-oncogene c-fes variant 3 [Homo sapiens (Hu...	193	1e-48
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<input type="checkbox"/>	sp_vs	P07948-2	Isoform LYN B of P07948 - Homo sapiens (Human) [L...	192	1e-48
<input type="checkbox"/>	tr	Q8WTZ8	_HUMAN RYK protein (Fragment) [RYK] [Homo sapiens (Human)]	192	2e-48
<input type="checkbox"/>	sp	P09619	PGFRB_HUMAN Beta-type platelet-derived growth factor r...	191	3e-48
<input type="checkbox"/>	sp	P07332	FES_HUMAN Proto-oncogene tyrosine-protein kinase Fes/F...	191	3e-48
<input type="checkbox"/>	tr	Q59F04	_HUMAN Platelet-derived growth factor receptor beta var...	191	3e-48
<input type="checkbox"/>	sp	P36888	FLT3_HUMAN FL cytokine receptor precursor (EC 2.7.10.1...	191	5e-48
<input type="checkbox"/>	tr	Q59EB3	_HUMAN Met proto-oncogene variant (Fragment) [Homo sapi...	191	5e-48

<input type="checkbox"/>	tr	A1L467	_HUMAN Met proto-oncogene (Hepatocyte growth factor rec...	191 5e-48
<input type="checkbox"/>	sp_vs	P21802-14	Isoform 14 of P21802 - Homo sapiens (Human) [FGF...	191 5e-48
<input type="checkbox"/>	tr	Q8NPA6	_HUMAN Transmembrane receptor PTK7-4 (PTK7 protein tyro...	190 6e-48
<input type="checkbox"/>	sp	Q04912	RON_HUMAN Macrophage-stimulating protein receptor prec...	189 1e-47
<input type="checkbox"/>	sp	P08581	MET_HUMAN Hepatocyte growth factor receptor precursor ...	189 1e-47
<input type="checkbox"/>	sp	P29376	LTK_HUMAN Leukocyte tyrosine kinase receptor precursor...	189 1e-47
<input type="checkbox"/>	tr	A6NNJ8	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	189 1e-47
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<input type="checkbox"/>	sp	Q05397	FAK1_HUMAN Focal adhesion kinase 1 (EC 2.7.10.2) (FADK...	188 2e-47
<input type="checkbox"/>	tr	Q8IYN9	_HUMAN PTK2 protein [PTK2] [Homo sapiens (Human)]	188 2e-47
<input type="checkbox"/>	tr	Q658W2	_HUMAN Putative uncharacterized protein DKFZp666O0110 [...	188 2e-47
<input type="checkbox"/>	sp	Q16832	DDR2_HUMAN Discoidin domain-containing receptor 2 prec...	188 3e-47
<input type="checkbox"/>	sp	Q01973	ROR1_HUMAN Tyrosine-protein kinase transmembrane recep...	187 4e-47
<input type="checkbox"/>	tr	Q72730	_HUMAN Discoidin domain receptor family, member 2 (Disc...	187 4e-47
<input type="checkbox"/>	tr	A2VCQ3	_HUMAN ROR1 protein (Fragment) [ROR1] [Homo sapiens (Hu...	187 4e-47
<input type="checkbox"/>	tr	Q6MZT2	_HUMAN Putative uncharacterized protein DKFZp686D1354 [...	187 5e-47
<input type="checkbox"/>	tr	Q8N9D7	_HUMAN CDNA FLJ37680 fis, clone BRHIP2012923, highly si...	186 9e-47
<input type="checkbox"/>	tr	Q59GN8	_HUMAN PTK2 protein tyrosine kinase 2 isoform b variant...	186 9e-47
<input type="checkbox"/>	tr	Q59GM6	_HUMAN PTK2 protein tyrosine kinase 2 isoform b variant...	186 9e-47
<input type="checkbox"/>	tr	Q12787	_HUMAN Receptor tyrosine kinase (Fragment) [Homo sapien...	186 9e-47
<input type="checkbox"/>	tr	Q5VTU6	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	185 2e-46
<input type="checkbox"/>	sp	Q13882	PTK6_HUMAN Tyrosine-protein kinase 6 (EC 2.7.10.2) (Br...	184 6e-46
<input type="checkbox"/>	sp	Q01974	ROR2_HUMAN Tyrosine-protein kinase transmembrane recep...	183 8e-46
<input type="checkbox"/>	tr	Q5VTT3	_HUMAN Receptor tyrosine kinase-like orphan receptor 2 ...	183 8e-46
<input type="checkbox"/>	tr	A6NNI9	_HUMAN Uncharacterized protein ROR2 [ROR2] [Homo sapien...	183 8e-46
<input type="checkbox"/>	tr	A1L4F5	_HUMAN Receptor tyrosine kinase-like orphan receptor 2 ...	183 8e-46
<input type="checkbox"/>	sp_vs	P06239-3	Isoform 3 of P06239 - Homo sapiens (Human) [LCK] ...	183 8e-46
<input type="checkbox"/>	sp	P12931	SRC_HUMAN Proto-oncogene tyrosine-protein kinase Src (...	182 2e-45
<input type="checkbox"/>	sp	P51813	BMX_HUMAN Cytoplasmic tyrosine-protein kinase BMX (EC ...	182 2e-45
<input type="checkbox"/>	tr	Q76P87	_HUMAN V-src sarcoma (Schmidt-Ruppin A-2) viral oncogen...	182 2e-45
<input type="checkbox"/>	sp_vs	P12931-2	Isoform 2 of P12931 - Homo sapiens (Human) [SRC] ...	182 2e-45
<input type="checkbox"/>	sp	P51451	BLK_HUMAN Tyrosine-protein kinase BLK (EC 2.7.10.2) (B...	182 2e-45
<input type="checkbox"/>	tr	Q96IN1	_HUMAN B lymphoid tyrosine kinase (B lymphoid tyrosine ...	182 2e-45
<input type="checkbox"/>	tr	Q96T35	_HUMAN Fibroblast growth factor receptor 3 IIIc isoform...	181 5e-45
<input type="checkbox"/>	tr	Q5R3A8	_HUMAN FYN oncogene related to SRC, FGR, YES [FYN] [Hom...	181 5e-45
<input type="checkbox"/>	tr	A6NIP9	_HUMAN Uncharacterized protein FYN [FYN] [Homo sapiens ...	181 5e-45
<input type="checkbox"/>	tr	Q6NSK4	_HUMAN DDR1 protein [DDR1] [Homo sapiens (Human)]	180 7e-45
<input type="checkbox"/>	tr	A6NP30	_HUMAN Uncharacterized protein PTK7 [PTK7] [Homo sapien...	180 9e-45
<input type="checkbox"/>	sp_vs	P06241-2	Isoform 2 of P06241 - Homo sapiens (Human) [FYN] ...	180 9e-45
<input type="checkbox"/>	sp	Q08345	DDR1_HUMAN Epithelial discoidin domain-containing rece...	179 1e-44
<input type="checkbox"/>	tr	Q5ST11	_HUMAN Discoidin domain receptor family, member 1 (Disc...	179 1e-44
<input type="checkbox"/>	tr	Q573B4	_HUMAN Proto-oncogene tyrosine-protein kinase LCK [LCK]...	179 1e-44
<input type="checkbox"/>	tr	Q4LE50	_HUMAN DDR1 variant protein (Fragment) [DDR1 variant pr...	179 1e-44
<input type="checkbox"/>	tr	Q2L6H3	_HUMAN Discoidin domain receptor family, member 1 (Disc...	179 1e-44
<input type="checkbox"/>	sp_vs	Q08345-2	Isoform 2 of Q08345 - Homo sapiens (Human) [DDR1]...	179 1e-44
<input type="checkbox"/>	sp	P07947	YES_HUMAN Proto-oncogene tyrosine-protein kinase Yes (...	179 1e-44
<input type="checkbox"/>	sp	P42680	TEC_HUMAN Tyrosine-protein kinase Tec (EC 2.7.10.2) [T...	178 3e-44
<input type="checkbox"/>	tr	A6NIH9	_HUMAN Uncharacterized protein BMX [BMX] [Homo sapiens ...	178 3e-44
<input type="checkbox"/>	sp	Q15375	EPHA7_HUMAN Ephrin type-A receptor 7 precursor (EC 2.7...	177 4e-44
<input type="checkbox"/>	tr	A6NLB3	_HUMAN Uncharacterized protein YES1 [YES1] [Homo sapien...	177 4e-44
<input type="checkbox"/>	sp_vs	Q15375-2	Isoform 2 of Q15375 - Homo sapiens (Human) [EPHA7...	177 4e-44
<input type="checkbox"/>	sp	P06241	FYN_HUMAN Proto-oncogene tyrosine-protein kinase Fyn (...	176 1e-43
<input type="checkbox"/>	sp	Q14289	FAK2_HUMAN Protein tyrosine kinase 2 beta (EC 2.7.10.2...	176 1e-43
<input type="checkbox"/>	sp	P29320	EPHA3_HUMAN Ephrin type-A receptor 3 precursor (EC 2.7...	176 1e-43
<input type="checkbox"/>	tr	Q6ZRA8	_HUMAN CDNA FLJ46514 fis, clone THYMU3032798, highly si...	176 1e-43
<input type="checkbox"/>	tr	Q6PID4	_HUMAN PTK2B protein tyrosine kinase 2 beta [PTK2B] [Ho...	176 1e-43
<input type="checkbox"/>	tr	Q6P4R6	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHA3] [Homo sapi...	176 1e-43
<input type="checkbox"/>	tr	Q59GM4	_HUMAN PTK2B protein tyrosine kinase 2 beta isoform a v...	176 1e-43
<input type="checkbox"/>	sp_vs	Q14289-2	Isoform 2 of Q14289 - Homo sapiens (Human) [PTK2B...	176 1e-43
<input type="checkbox"/>	sp_vs	Q05397-2	Isoform 2 of Q05397 - Homo sapiens (Human) [PTK2]...	176 1e-43
<input type="checkbox"/>	sp	P04626	ERBB2_HUMAN Receptor tyrosine-protein kinase erbB-2 pr...	176 2e-43
<input type="checkbox"/>	tr	Q05D26	_HUMAN BLK protein (Fragment) [BLK] [Homo sapiens (Human)]	176 2e-43
<input type="checkbox"/>	sp	P09769	FGR_HUMAN Proto-oncogene tyrosine-protein kinase FGR (...	175 2e-43
<input type="checkbox"/>	sp	Q15303	ERBB4_HUMAN Receptor tyrosine-protein kinase erbB-4 pr...	175 2e-43
<input type="checkbox"/>	sp_vs	Q15303-2	Isoform JM-B of Q15303 - Homo sapiens (Human) [ER...	175 2e-43

<input type="checkbox"/>	sp_vs	Q15303-3	Isoform 3 of Q15303 - Homo sapiens (Human) [ERBB4...	175	2e-43
<input type="checkbox"/>	sp	P29322	EPHA8_HUMAN Ephrin type-A receptor 8 precursor (EC 2.7...	175	3e-43
<input type="checkbox"/>	sp_vs	Q05397-3	Isoform 3 of Q05397 - Homo sapiens (Human) [PTK2]...	174	5e-43
<input type="checkbox"/>	sp	P54756	EPHA5_HUMAN Ephrin type-A receptor 5 precursor (EC 2.7...	174	6e-43
<input type="checkbox"/>	sp	P29317	EPHA2_HUMAN Ephrin type-A receptor 2 precursor (EC 2.7...	174	6e-43
<input type="checkbox"/>	tr	Q8N3Z2	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHA2] [Homo sapi...	174	6e-43
<input type="checkbox"/>	tr	Q59FT4	_HUMAN Ephrin receptor (EC 2.7.10.1) (Fragment) [Homo s...	174	6e-43
<input type="checkbox"/>	tr	A2ABL4	_HUMAN Discoidin domain receptor family, member 1 (Frag...	174	6e-43
<input type="checkbox"/>	sp_vs	P54756-2	Isoform 2 of P54756 - Homo sapiens (Human) [EPHA5...	174	6e-43
<input type="checkbox"/>	sp	P54764	EPHA4_HUMAN Ephrin type-A receptor 4 precursor (EC 2.7...	171	3e-42
<input type="checkbox"/>	sp	P21709	EPHA1_HUMAN Ephrin type-A receptor 1 precursor (EC 2.7...	171	3e-42
<input type="checkbox"/>	tr	Q58F15	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHA4] [Homo sapi...	171	3e-42
<input type="checkbox"/>	tr	Q53TA0	_HUMAN Putative uncharacterized protein EPHA4 (Fragment...	171	3e-42
<input type="checkbox"/>	tr	A1L3V3	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHA1] [Homo sapi...	171	3e-42
<input type="checkbox"/>	tr	Q9NSQ6	_HUMAN Putative uncharacterized protein DKFZp434L0319 (...	171	5e-42
<input type="checkbox"/>	tr	Q7Z3F2	_HUMAN Ephrin receptor (EC 2.7.10.1) [DKFZp686C0686] [H...	171	5e-42
<input type="checkbox"/>	sp	P29323	EPHB2_HUMAN Ephrin type-B receptor 2 precursor (EC 2.7...	169	2e-41
<input type="checkbox"/>	tr	Q5TFU3	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHB2] [Homo sapi...	169	2e-41
<input type="checkbox"/>	tr	Q4LE53	_HUMAN Ephrin receptor (EC 2.7.10.1) (Fragment) [EPHB2 ...	169	2e-41
<input type="checkbox"/>	tr	A6NJM0	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHB2] [Homo sapi...	169	2e-41
<input type="checkbox"/>	sp_vs	P29323-2	Isoform 2 of P29323 - Homo sapiens (Human) [EPHB2...	169	2e-41
<input type="checkbox"/>	sp_vs	P29323-3	Isoform 3 of P29323 - Homo sapiens (Human) [EPHB2...	169	2e-41
<input type="checkbox"/>	sp	Q06187	BTX_HUMAN Tyrosine-protein kinase BTK (EC 2.7.10.2) (B...	169	2e-41
<input type="checkbox"/>	sp	P00533	EGFR_HUMAN Epidermal growth factor receptor precursor ...	168	3e-41
<input type="checkbox"/>	tr	Q59FL8	_HUMAN Epidermal growth factor receptor isoform a varia...	168	3e-41
<input type="checkbox"/>	tr	Q504U0	_HUMAN EGFR protein [EGFR] [Homo sapiens (Human)]	168	3e-41
<input type="checkbox"/>	tr	Q2TTR7	_HUMAN Cell growth inhibiting protein 40 [Homo sapiens ...	168	3e-41
<input type="checkbox"/>	tr	Q4JFK8	_HUMAN Fes/fps proto-oncogene (Fragment) [FES] [Homo sa...	168	3e-41
<input type="checkbox"/>	tr	Q59GQ2	_HUMAN Tyrosine-protein kinase (EC 2.7.10.2) (Fragment)...	167	4e-41
<input type="checkbox"/>	sp	P42681	TXK_HUMAN Tyrosine-protein kinase TXK (EC 2.7.10.2) [T...	167	6e-41
<input type="checkbox"/>	sp	O60674	JAK2_HUMAN Tyrosine-protein kinase JAK2 (EC 2.7.10.2) ...	166	1e-40
<input type="checkbox"/>	tr	Q8IXP2	_HUMAN Tyrosine-protein kinase (EC 2.7.10.2) [JAK2] [Ho...	166	1e-40
<input type="checkbox"/>	tr	Q506Q0	_HUMAN Tyrosine-protein kinase (EC 2.7.10.2) [JAK2] [Ho...	166	1e-40
<input type="checkbox"/>	sp	P54762	EPHB1_HUMAN Ephrin type-B receptor 1 precursor (EC 2.7...	166	1e-40
<input type="checkbox"/>	sp_vs	P54762-2	Isoform 2 of P54762 - Homo sapiens (Human) [EPHB1...	166	1e-40
<input type="checkbox"/>	tr	Q0VG87	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHB1] [Homo sapi...	165	3e-40
<input type="checkbox"/>	sp	P23458	JAK1_HUMAN Tyrosine-protein kinase JAK1 (EC 2.7.10.2) ...	164	4e-40
<input type="checkbox"/>	sp	P43405	KSYK_HUMAN Tyrosine-protein kinase SYK (EC 2.7.10.2) (...	164	6e-40
<input type="checkbox"/>	tr	Q5T6N8	_HUMAN Spleen tyrosine kinase (Spleen tyrosine kinase, ...	164	6e-40
<input type="checkbox"/>	tr	Q5T6N7	_HUMAN Spleen tyrosine kinase (Spleen tyrosine kinase, ...	164	6e-40
<input type="checkbox"/>	tr	Q59FQ5	_HUMAN RYK receptor-like tyrosine kinase isoform 1 vari...	164	6e-40
<input type="checkbox"/>	sp_vs	P43405-2	Isoform Short of P43405 - Homo sapiens (Human) [S...	164	6e-40
<input type="checkbox"/>	sp	P54760	EPHB4_HUMAN Ephrin type-B receptor 4 precursor (EC 2.7...	163	8e-40
<input type="checkbox"/>	tr	Q96L35	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHB4] [Homo sapi...	163	8e-40
<input type="checkbox"/>	tr	Q7Z635	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHB4] [Homo sapi...	163	8e-40
<input type="checkbox"/>	tr	Q59P17	_HUMAN Ephrin receptor (EC 2.7.10.1) (Fragment) [Homo s...	163	8e-40
<input type="checkbox"/>	tr	Q541P7	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHB4] [Homo sapi...	163	8e-40
<input type="checkbox"/>	sp	Q08881	ITK_HUMAN Tyrosine-protein kinase ITK/TSK (EC 2.7.10.2...	163	1e-39
<input type="checkbox"/>	tr	Q9UMB0	_HUMAN Fibroblast growth factor receptor-related protei...	162	1e-39
<input type="checkbox"/>	tr	Q9H7V3	_HUMAN CDNA FLJ14219 fis, clone NT2RP3003800, highly si...	162	2e-39
<input type="checkbox"/>	sp	P43403	ZAP70_HUMAN Tyrosine-protein kinase ZAP-70 (EC 2.7.10....	160	5e-39
<input type="checkbox"/>	tr	Q6PIA4	_HUMAN ZAP70 protein (Putative uncharacterized protein ...	160	5e-39
<input type="checkbox"/>	sp	P54753	EPHB3_HUMAN Ephrin type-B receptor 3 precursor (EC 2.7...	160	7e-39
<input type="checkbox"/>	sp_vs	P06241-3	Isoform 3 of P06241 - Homo sapiens (Human) [FYN] ...	160	9e-39
<input type="checkbox"/>	sp_vs	Q01973-2	Isoform Short of Q01973 - Homo sapiens (Human) [R...	160	9e-39
<input type="checkbox"/>	sp	Q6J9G0	STYK1_HUMAN Tyrosine protein-kinase STYK1 (EC 2.7.10.2...	158	4e-38
<input type="checkbox"/>	sp	Q07912	ACK1_HUMAN Activated CDC42 kinase 1 (EC 2.7.10.2) (ACK...	156	1e-37
<input type="checkbox"/>	tr	Q6ZMQ0	_HUMAN CDNA FLJ16772 fis, clone BRAWH3043827, highly si...	156	1e-37
<input type="checkbox"/>	sp_vs	Q07912-2	Isoform 2 of Q07912 - Homo sapiens (Human) [TNK2]...	156	1e-37
<input type="checkbox"/>	sp	P29597	TYK2_HUMAN Non-receptor tyrosine-protein kinase TYK2 (...	155	2e-37
<input type="checkbox"/>	tr	Q2VKS9	_HUMAN Proto-oncogene c-fes variant 2 [Homo sapiens (Hu...	155	2e-37
<input type="checkbox"/>	tr	Q8IXD6	_HUMAN Truncated ZAP kinase [Homo sapiens (Human)]	155	2e-37
<input type="checkbox"/>	tr	Q6LBK2	_HUMAN Acidic fibroblast growth factor (Fragment) [FGFR...	155	2e-37
<input type="checkbox"/>	tr	Q4LXD3	_HUMAN Janus kinase 1 [JAK1] [Homo sapiens (Human)]	154	5e-37
<input type="checkbox"/>	tr	Q96T34	_HUMAN Fibroblast growth factor receptor 3 IIIC isoform...	154	7e-37
<input type="checkbox"/>	tr	A6NFP4	_HUMAN Uncharacterized protein ZAP70 [ZAP70] [Homo sapi...	154	7e-37

<input type="checkbox"/>	tr	Q53T57	_HUMAN Putative uncharacterized protein ERBB4 (Fragment)...	152	2e-36
<input type="checkbox"/>	sp	P52333	JAK3_HUMAN Tyrosine-protein kinase JAK3 (EC 2.7.10.2) ...	152	3e-36
<input type="checkbox"/>	tr	Q99699	_HUMAN Tyrosine-protein kinase (EC 2.7.10.2) [JAK3] [Ho...	152	3e-36
<input type="checkbox"/>	tr	Q75MF2	_HUMAN Putative uncharacterized protein EGFR (Fragment)...	150	1e-35
<input type="checkbox"/>	tr	Q59FX1	_HUMAN Putative uncharacterized protein (Fragment) [Hom...	150	1e-35
<input type="checkbox"/>	sp	P21860	ERBB3_HUMAN Receptor tyrosine-protein kinase erbB-3 pr...	148	4e-35
<input type="checkbox"/>	tr	Q15516	_HUMAN Tyrosine kinase [Homo sapiens (Human)]	147	6e-35
<input type="checkbox"/>	sp	Q5JZY3	EPHAA_HUMAN Ephrin type-A receptor 10 precursor (EC 2...	145	2e-34
<input type="checkbox"/>	tr	Q3MS96	_HUMAN Dominant-negative kinase-deficient Brutons tyros...	145	2e-34
<input type="checkbox"/>	sp	Q9UF33	EPHA6_HUMAN Ephrin type-A receptor 6 precursor (EC 2.7...	144	7e-34
<input type="checkbox"/>	tr	Q6ZNH1	_HUMAN CDNA FLJ16103 fis, clone TESTI2016663, moderatel...	144	7e-34
<input type="checkbox"/>	sp_vs	P54762-3	Isoform 3 of P54762 - Homo sapiens (Human) [EPHB1...	142	3e-33
<input type="checkbox"/>	tr	Q96HF4	_HUMAN EPHA2 protein (Fragment) [EPHA2] [Homo sapiens (...]	141	3e-33
<input type="checkbox"/>	sp	Q96Q04	LMTK3_HUMAN Serine/threonine-protein kinase LMTK3 prec...	135	2e-31
<input type="checkbox"/>	sp	Q12852	M3K12_HUMAN Mitogen-activated protein kinase kinase ki...	134	5e-31
<input type="checkbox"/>	sp	Q8N441	FGRL1_HUMAN Fibroblast growth factor receptor-like 1 p...	133	9e-31
<input type="checkbox"/>	tr	Q9P0L3	_HUMAN Bruton's tyrosine kinase (Fragment) [Homo sapien...	133	9e-31
<input type="checkbox"/>	tr	Q6ZMD4	_HUMAN CDNA FLJ23990 fis, clone HRC08053, highly simila...	133	9e-31
<input type="checkbox"/>	tr	A4FU89	_HUMAN EPHA10 protein [EPHA10] [Homo sapiens (Human)]	132	2e-30
<input type="checkbox"/>	sp_vs	Q5JZY3-3	Isoform 3 of Q5JZY3 - Homo sapiens (Human) [EPHA1...	132	2e-30
<input type="checkbox"/>	tr	Q3MS92	_HUMAN Dominant-negative kinase-deficient Brutons tyros...	132	3e-30
<input type="checkbox"/>	tr	Q9P0L5	_HUMAN Bruton's tyrosine kinase [Homo sapiens (Human)]	131	5e-30
<input type="checkbox"/>	sp_vs	P52333-2	Isoform 1 of P52333 - Homo sapiens (Human) [JAK3]...	131	5e-30
<input type="checkbox"/>	sp_vs	P52333-3	Isoform 3 of P52333 - Homo sapiens (Human) [JAK3]...	131	5e-30
<input type="checkbox"/>	sp	Q13470	TNK1_HUMAN Non-receptor tyrosine-protein kinase TNK1 (...]	130	8e-30
<input type="checkbox"/>	tr	Q9P0L7	_HUMAN Bruton's tyrosine kinase [Homo sapiens (Human)]	130	8e-30
<input type="checkbox"/>	tr	Q9P0L6	_HUMAN Bruton's tyrosine kinase [Homo sapiens (Human)]	130	8e-30
<input type="checkbox"/>	sp_vs	Q13470-2	Isoform 2 of Q13470 - Homo sapiens (Human) [TNK1]...	130	8e-30
<input type="checkbox"/>	tr	Q9NPI3	_HUMAN Bruton's tyrosine kinase [Homo sapiens (Human)]	130	1e-29
<input type="checkbox"/>	tr	Q9NPI2	_HUMAN Bruton's tyrosine kinase [Homo sapiens (Human)]	130	1e-29
<input type="checkbox"/>	sp	Q9NYL2	MLTK_HUMAN Mitogen-activated protein kinase kinase kin...	129	2e-29
<input type="checkbox"/>	sp	O43283	M3K13_HUMAN Mitogen-activated protein kinase kinase ki...	129	2e-29
<input type="checkbox"/>	sp_vs	Q9NYL2-2	Isoform 2 of Q9NYL2 - Homo sapiens (Human) [MLTK]...	129	2e-29
<input type="checkbox"/>	sp_vs	Q9NYL2-3	Isoform 3 of Q9NYL2 - Homo sapiens (Human) [MLTK]...	129	2e-29
<input type="checkbox"/>	tr	Q59GJ1	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) (...]	129	2e-29
<input type="checkbox"/>	sp	Q02779	M3K10_HUMAN Mitogen-activated protein kinase kinase ki...	128	4e-29
<input type="checkbox"/>	sp	P80192	M3K9_HUMAN Mitogen-activated protein kinase kinase kin...	127	5e-29
<input type="checkbox"/>	tr	A3KN85	_HUMAN MAP3K9 protein [MAP3K9] [Homo sapiens (Human)]	127	5e-29
<input type="checkbox"/>	sp_vs	P80192-4	Isoform 2 of P80192 - Homo sapiens (Human) [MAP3K...	127	5e-29
<input type="checkbox"/>	sp	Q6ZMQ8	LMTK1_HUMAN Serine/threonine-protein kinase LMTK1 (EC ...]	124	4e-28
<input type="checkbox"/>	tr	Q6P4H5	_HUMAN PDGFRA protein [PDGFRA] [Homo sapiens (Human)]	124	4e-28
<input type="checkbox"/>	sp_vs	Q6ZMQ8-3	Isoform 3 of Q6ZMQ8 - Homo sapiens (Human) [AATK]...	124	4e-28
<input type="checkbox"/>	sp	Q5TCX8	M3KL4_HUMAN Mitogen-activated protein kinase kinase ki...	123	1e-27
<input type="checkbox"/>	sp	Q16584	M3K11_HUMAN Mitogen-activated protein kinase kinase ki...	123	1e-27
<input type="checkbox"/>	sp_vs	Q5TCX8-2	Isoform 2 of Q5TCX8 - Homo sapiens (Human) [MLK4]...	123	1e-27
<input type="checkbox"/>	sp	Q15197	EPHB6_HUMAN Ephrin type-B receptor 6 precursor (Tyrosi...	122	2e-27
<input type="checkbox"/>	tr	Q2TB24	_HUMAN EPHB6 protein (EPH receptor B6, isoform CRA_b) [...]	122	2e-27
<input type="checkbox"/>	tr	Q2TB23	_HUMAN EPH receptor B6 (EphB6) [EPHB6] [Homo sapiens (H...	122	2e-27
<input type="checkbox"/>	tr	Q9UMA9	_HUMAN Fibroblast growth factor receptor (Fragment) [BE...	122	3e-27
<input type="checkbox"/>	tr	Q9P0M0	_HUMAN Bruton's tyrosine kinase [Homo sapiens (Human)]	121	4e-27
<input type="checkbox"/>	sp	O43318	M3K7_HUMAN Mitogen-activated protein kinase kinase kin...	113	1e-24
<input type="checkbox"/>	tr	Q9NZ70	_HUMAN TGF beta-activated kinase splice variant d (Mito...	113	1e-24
<input type="checkbox"/>	tr	Q5U0D0	_HUMAN Mitogen-activated protein kinase kinase kinase 7...	113	1e-24
<input type="checkbox"/>	tr	Q5TDM9	_HUMAN Mitogen-activated protein kinase kinase kinase 7...	113	1e-24
<input type="checkbox"/>	sp_vs	O43318-2	Isoform 1A of O43318 - Homo sapiens (Human) [MAP3...	113	1e-24
<input type="checkbox"/>	sp_vs	O43318-3	Isoform 1C of O43318 - Homo sapiens (Human) [MAP3...	113	1e-24
<input type="checkbox"/>	tr	Q5U0C9	_HUMAN Mitogen-activated protein kinase kinase kinase 7...	112	2e-24
<input type="checkbox"/>	tr	Q5JY90	_HUMAN Bruton agammaglobulinemia tyrosine kinase (Bruto...	110	8e-24
<input type="checkbox"/>	sp	P04049	RAF1_HUMAN RAF proto-oncogene serine/threonine-protein...	104	5e-22
<input type="checkbox"/>	tr	Q59HE0	_HUMAN Colony stimulating factor 1 receptor variant (Fr...	104	5e-22
<input type="checkbox"/>	tr	Q15278	_HUMAN RAF1 protein (Fragment) [RAF1] [Homo sapiens (Hu...	104	5e-22
<input type="checkbox"/>	sp	Q13546	RIPK1_HUMAN Receptor-interacting serine/threonine-prot...	103	8e-22
<input type="checkbox"/>	sp	Q8IWU2	LMTK2_HUMAN Serine/threonine-protein kinase LMTK2 prec...	103	1e-21
<input type="checkbox"/>	tr	A4D272	_HUMAN Lemur tyrosine kinase 2 (Lemur tyrosine kinase 2...	103	1e-21
<input type="checkbox"/>	sp	P15056	BRAF1_HUMAN B-Raf proto-oncogene serine/threonine-prot...	102	2e-21
<input type="checkbox"/>	tr	Q5IBP5	_HUMAN AKAP9-BRAF fusion protein [Homo sapiens (Human)]	102	2e-21

<input type="checkbox"/>	tr	A4D1T4	_HUMAN V-raf murine sarcoma viral oncogene homolog B1 [...	102	2e-21
<input type="checkbox"/>	tr	Q5UBV6	_HUMAN NIN/PDGFRB fusion protein (Fragment) [NIN/PDGFRB...	102	3e-21
<input type="checkbox"/>	sp	P53667	LIMK1_HUMAN LIM domain kinase 1 (EC 2.7.11.1) (LIMK-1)...	101	5e-21
<input type="checkbox"/>	sp_vs	P53667-2	Isoform 2 of P53667 - Homo sapiens (Human) [LIMK1...	101	5e-21
<input type="checkbox"/>	sp	P10398	ARAF_HUMAN A-Raf proto-oncogene serine/threonine-prote...	100	7e-21
<input type="checkbox"/>	tr	Q96II5	_HUMAN ARAF protein [ARAF] [Homo sapiens (Human)]	100	7e-21
<input type="checkbox"/>	tr	Q8TCG9	_HUMAN KIT protein (Fragment) [KIT] [Homo sapiens (Human)]	100	9e-21
<input type="checkbox"/>	sp	Q96S53	TESK2_HUMAN Dual specificity testis-specific protein k...	99	2e-20
<input type="checkbox"/>	tr	Q5T152	_HUMAN Testis-specific kinase 2 (Testis-specific kinase...	99	2e-20
<input type="checkbox"/>	sp	Q9Y6E0	STK24_HUMAN Serine/threonine-protein kinase 24 (EC 2.7...	99	3e-20
<input type="checkbox"/>	tr	Q6P0Y1	_HUMAN Serine/threonine kinase 24 (STE20 homolog, yeast...	99	3e-20
<input type="checkbox"/>	tr	Q5U0E6	_HUMAN Serine/threonine kinase 24 (STE20 homolog, yeast...	99	3e-20
<input type="checkbox"/>	tr	Q5T5B3	_HUMAN Serine/threonine kinase 24 (STE20 homolog, yeast...	99	3e-20
<input type="checkbox"/>	tr	A0PJ49	_HUMAN FGFR1 protein (Fragment) [FGFR1] [Homo sapiens...	99	3e-20
<input type="checkbox"/>	sp_vs	Q9Y6E0-2	Isoform A of Q9Y6E0 - Homo sapiens (Human) [STK24...	99	3e-20
<input type="checkbox"/>	sp	Q04759	KPCT_HUMAN Protein kinase C theta type (EC 2.7.11.13) ...	98	4e-20
<input type="checkbox"/>	tr	Q9UDF1	_HUMAN Fibroblast growth factor receptor 1 THIRD immuno...	98	4e-20
<input type="checkbox"/>	tr	Q5JUN8	_HUMAN Protein kinase C, theta (Fragment) [PRKCQ] [Homo...	98	4e-20
<input type="checkbox"/>	sp	Q6P3R8	NEK5_HUMAN Serine/threonine-protein kinase Nek5 (EC 2....	97	1e-19
<input type="checkbox"/>	tr	Q6PG81	_HUMAN STK24 protein (Fragment) [STK24] [Homo sapiens (...	97	1e-19
<input type="checkbox"/>	tr	A6NIT1	_HUMAN Uncharacterized protein ARAF [ARAF] [Homo sapien...	96	2e-19
<input type="checkbox"/>	sp	Q15416	KS6A1_HUMAN Ribosomal protein S6 kinase alpha-1 (EC 2....	95	4e-19
<input type="checkbox"/>	tr	A6NGG4	_HUMAN Uncharacterized protein RPS6KA1 [RPS6KA1] [Homo ...	95	4e-19
<input type="checkbox"/>	tr	A6NFC2	_HUMAN Uncharacterized protein ERBB2 [ERBB2] [Homo sapi...	95	5e-19
<input type="checkbox"/>	sp	Q9H2G2	SLK_HUMAN STE20-like serine/threonine-protein kinase (...	94	8e-19
<input type="checkbox"/>	sp	Q9P0L2	MARK1_HUMAN Serine/threonine-protein kinase MARK1 (EC ...	94	8e-19
<input type="checkbox"/>	sp_vs	Q9H2G2-2	Isoform 2 of Q9H2G2 - Homo sapiens (Human) [SLK] ...	94	8e-19
<input type="checkbox"/>	sp_vs	P27448-3	Isoform 3 of P27448 - Homo sapiens (Human) [MARK3...	94	1e-18
<input type="checkbox"/>	sp_vs	P27448-4	Isoform 4 of P27448 - Homo sapiens (Human) [MARK3...	94	1e-18
<input type="checkbox"/>	sp_vs	P27448-5	Isoform 5 of P27448 - Homo sapiens (Human) [MARK3...	94	1e-18
<input type="checkbox"/>	sp_vs	P27448-6	Isoform 6 of P27448 - Homo sapiens (Human) [MARK3...	94	1e-18
<input type="checkbox"/>	tr	Q14219	_HUMAN Protein tyrosine kinase (Fragment) [tec] [Homo s...	93	1e-18
<input type="checkbox"/>	sp	Q7KZI7	MARK2_HUMAN Serine/threonine-protein kinase MARK2 (EC ...	93	2e-18
<input type="checkbox"/>	sp_vs	Q7KZI7-2	Isoform 2 of Q7KZI7 - Homo sapiens (Human) [MARK2...	93	2e-18
<input type="checkbox"/>	sp_vs	Q7KZI7-3	Isoform 3 of Q7KZI7 - Homo sapiens (Human) [MARK2...	93	2e-18
<input type="checkbox"/>	sp_vs	Q7KZI7-4	Isoform 4 of Q7KZI7 - Homo sapiens (Human) [MARK2...	93	2e-18
<input type="checkbox"/>	sp_vs	Q7KZI7-5	Isoform 5 of Q7KZI7 - Homo sapiens (Human) [MARK2...	93	2e-18
<input type="checkbox"/>	sp_vs	Q7KZI7-6	Isoform 6 of Q7KZI7 - Homo sapiens (Human) [MARK2...	93	2e-18
<input type="checkbox"/>	sp_vs	Q7KZI7-7	Isoform 7 of Q7KZI7 - Homo sapiens (Human) [MARK2...	93	2e-18
<input type="checkbox"/>	sp_vs	Q7KZI7-8	Isoform 8 of Q7KZI7 - Homo sapiens (Human) [MARK2...	93	2e-18
<input type="checkbox"/>	sp_vs	Q7KZI7-9	Isoform 9 of Q7KZI7 - Homo sapiens (Human) [MARK2...	93	2e-18
<input type="checkbox"/>	sp_vs	Q7KZI7-10	Isoform 10 of Q7KZI7 - Homo sapiens (Human) [MAR...	93	2e-18
<input type="checkbox"/>	sp_vs	Q7KZI7-11	Isoform 11 of Q7KZI7 - Homo sapiens (Human) [MAR...	93	2e-18
<input type="checkbox"/>	sp_vs	Q7KZI7-12	Isoform 12 of Q7KZI7 - Homo sapiens (Human) [MAR...	93	2e-18
<input type="checkbox"/>	sp	Q15569	TESK1_HUMAN Dual specificity testis-specific protein k...	92	3e-18
<input type="checkbox"/>	tr	Q8IXZ8	_HUMAN TESK1 protein (Testis-specific kinase 1, isoform...	92	3e-18
<input type="checkbox"/>	tr	Q59FZ4	_HUMAN Serine/threonine kinase 4 variant (Fragment) [Ho...	92	3e-18
<input type="checkbox"/>	sp	Q8TDX7	NEK7_HUMAN Serine/threonine-protein kinase Nek7 (EC 2....	91	5e-18
<input type="checkbox"/>	sp	P05771	KPCB_HUMAN Protein kinase C beta type (EC 2.7.11.13) (...	91	5e-18
<input type="checkbox"/>	tr	A6NH24	_HUMAN Uncharacterized protein ROBO1 [ROBO1] [Homo sapi...	91	5e-18
<input type="checkbox"/>	sp_vs	P05771-2	Isoform Beta-II of P05771 - Homo sapiens (Human) ...	91	5e-18
<input type="checkbox"/>	sp	Q15349	KS6A2_HUMAN Ribosomal protein S6 kinase alpha-2 (EC 2....	91	7e-18
<input type="checkbox"/>	tr	Q05DF6	_HUMAN NEK4 protein (Fragment) [NEK4] [Homo sapiens (Hu...	91	7e-18
<input type="checkbox"/>	tr	A6NND1	_HUMAN Uncharacterized protein RPS6KA2 [RPS6KA2] [Homo ...	91	7e-18
<input type="checkbox"/>	sp_vs	Q05397-4	Isoform 4 of Q05397 - Homo sapiens (Human) [PTK2]...	91	7e-18
<input type="checkbox"/>	sp_vs	Q15349-2	Isoform 2 of Q15349 - Homo sapiens (Human) [RPS6K...	91	7e-18
<input type="checkbox"/>	sp	Q9Y6N7	ROBO1_HUMAN Roundabout homolog 1 precursor (H-Robo-1) ...	91	9e-18
<input type="checkbox"/>	sp	P51957	NEK4_HUMAN Serine/threonine-protein kinase Nek4 (EC 2....	91	9e-18
<input type="checkbox"/>	sp	P51812	KS6A3_HUMAN Ribosomal protein S6 kinase alpha-3 (EC 2....	91	9e-18
<input type="checkbox"/>	tr	Q6P576	_HUMAN NEK4 protein [Homo sapiens (Human)]	91	9e-18
<input type="checkbox"/>	sp_vs	Q9Y6N7-2	Isoform 2 of Q9Y6N7 - Homo sapiens (Human) [ROBO1...	91	9e-18
<input type="checkbox"/>	sp	Q9UEW8	STK39_HUMAN STE20/SPS1-related proline-alanine-rich pr...	90	1e-17
<input type="checkbox"/>	tr	Q53390	_HUMAN Putative uncharacterized protein STK39 (Fragment...	90	1e-17
<input type="checkbox"/>	sp	P27448	MARK3_HUMAN MAP/microtubule affinity-regulating kinase...	90	2e-17
<input type="checkbox"/>	sp_vs	P27448-2	Isoform 2 of P27448 - Homo sapiens (Human) [MARK3...	90	2e-17
<input type="checkbox"/>	sp_vs	P27448-7	Isoform 7 of P27448 - Homo sapiens (Human) [MARK3...	90	2e-17

<input type="checkbox"/>	tr	Q8NFEJ4	_HUMAN Testis-specific kinase-1 (Fragment) [Homo sapien...	89 2e-17
<input type="checkbox"/>	tr	Q6NSKO	_HUMAN Serine/threonine kinase 10 [STK10] [Homo sapiens...	89 2e-17
<input type="checkbox"/>	tr	Q2M1J3	_HUMAN ROBO1 protein [ROBO1] [Homo sapiens (Human)]	89 2e-17
<input type="checkbox"/>	tr	Q1RMC8	_HUMAN ROBO1 protein [ROBO1] [Homo sapiens (Human)]	89 2e-17
<input type="checkbox"/>	tr	Q1RMC7	_HUMAN ROBO1 protein [ROBO1] [Homo sapiens (Human)]	89 2e-17
<input type="checkbox"/>	sp_vs	Q9Y6N7-3	Isoform 3 of Q9Y6N7 - Homo sapiens (Human) [ROBO1...	89 2e-17
<input type="checkbox"/>	sp	Q9H0K1	SN1L2_HUMAN Serine/threonine-protein kinase SNF1-like ...	89 3e-17
<input type="checkbox"/>	sp	Q9H093	NUAK2_HUMAN NUA family SNF1-like kinase 2 (EC 2.7.11....	89 3e-17
<input type="checkbox"/>	sp	Q9P289	MST4_HUMAN Serine/threonine-protein kinase MST4 (EC 2....	89 3e-17
<input type="checkbox"/>	tr	Q8NBY1	_HUMAN CDNA FLJ90669 fis, clone PLACE1005519, moderatel...	89 3e-17
<input type="checkbox"/>	tr	Q499L9	_HUMAN Serine/threonine protein kinase MST4 [MST4] [Hom...	89 3e-17
<input type="checkbox"/>	sp	Q9NRP7	STK36_HUMAN Serine/threonine-protein kinase 36 (EC 2.7...	89 3e-17
<input type="checkbox"/>	sp	P51956	NEK3_HUMAN Serine/threonine-protein kinase Nek3 (EC 2....	89 3e-17
<input type="checkbox"/>	tr	Q6ZN64	_HUMAN CDNA FLJ16392 fis, clone TRACH2020048, moderatel...	89 3e-17
<input type="checkbox"/>	tr	Q5TAP2	_HUMAN NIMA (Never in mitosis gene a)-related kinase 3 ...	89 3e-17
<input type="checkbox"/>	tr	Q5T153	_HUMAN Testis-specific kinase 2 [TESK2] [Homo sapiens (...	89 3e-17
<input type="checkbox"/>	tr	P78483	_HUMAN C-src-2 protein (Fragment) [FGR] [Homo sapiens (...	89 3e-17
<input type="checkbox"/>	tr	ASYM70	_HUMAN NEK4 protein [NEK4] [Homo sapiens (Human)]	89 3e-17
<input type="checkbox"/>	sp_vs	Q9NRP7-2	Isoform 2 of Q9NRP7 - Homo sapiens (Human) [STK36...	89 3e-17
<input type="checkbox"/>	sp_vs	Q96S53-3	Isoform 3 of Q96S53 - Homo sapiens (Human) [TESK2...	89 3e-17
<input type="checkbox"/>	tr	Q9UEH2	_HUMAN BEK fibroblast growth factor receptor (Fragment)...	88 4e-17
<input type="checkbox"/>	tr	Q8J023	_HUMAN NIMA-related protein kinase 3 [NEK3] [Homo sapie...	88 4e-17
<input type="checkbox"/>	tr	Q572P5	_HUMAN Tyrosine-protein kinase BTK isoform 65 (Fragment...	88 4e-17
<input type="checkbox"/>	tr	Q08AF4	_HUMAN PKN2 protein [PKN2] [Homo sapiens (Human)]	88 4e-17
<input type="checkbox"/>	sp	Q13043	STK4_HUMAN Serine/threonine-protein kinase 4 (EC 2.7.1...	88 6e-17
<input type="checkbox"/>	sp	Q94804	STK10_HUMAN Serine/threonine-protein kinase 10 (EC 2.7...	88 6e-17
<input type="checkbox"/>	sp	P53671	LIMK2_HUMAN LIM domain kinase 2 (EC 2.7.11.1) (LIMK-2)...	88 6e-17
<input type="checkbox"/>	tr	Q9UFU0	_HUMAN Putative uncharacterized protein DKFZp586K0922 (...	88 6e-17
<input type="checkbox"/>	tr	A6ND35	_HUMAN Uncharacterized protein STK10 [STK10] [Homo sapi...	88 6e-17
<input type="checkbox"/>	tr	A0PJ51	_HUMAN STK4 protein (Fragment) [STK4] [Homo sapiens (Hu...	88 6e-17
<input type="checkbox"/>	sp_vs	P53671-2	Isoform LIMK2b of P53671 - Homo sapiens (Human) [...	88 6e-17
<input type="checkbox"/>	sp_vs	Q13043-2	Isoform 2 of Q13043 - Homo sapiens (Human) [STK4]...	88 6e-17
<input type="checkbox"/>	sp	Q16513	PKN2_HUMAN Serine/threonine-protein kinase N2 (EC 2.7....	87 8e-17
<input type="checkbox"/>	sp	Q96PY6	NEK1_HUMAN Serine/threonine-protein kinase Nek1 (EC 2....	87 8e-17
<input type="checkbox"/>	sp	Q96RW7	HMCN1_HUMAN Hemicentin-1 precursor (Fibulin-6) (FIBL-6...	87 8e-17
<input type="checkbox"/>	tr	Q86XJ6	_HUMAN Protein kinase C, delta (Protein kinase C, delta...	87 8e-17
<input type="checkbox"/>	tr	Q14CB7	_HUMAN NEK1 protein [NEK1] [Homo sapiens (Human)]	87 8e-17
<input type="checkbox"/>	tr	Q05DG5	_HUMAN NEK1 protein (Fragment) [NEK1] [Homo sapiens (Hu...	87 8e-17
<input type="checkbox"/>	tr	A6NGE3	_HUMAN Uncharacterized protein HMCN1 [HMCN1] [Homo sapi...	87 8e-17
<input type="checkbox"/>	sp_vs	Q96RW7-2	Isoform 2 of Q96RW7 - Homo sapiens (Human) [HMCN1...	87 8e-17
<input type="checkbox"/>	sp_vs	Q96PY6-2	Isoform 2 of Q96PY6 - Homo sapiens (Human) [NEK1]...	87 8e-17
<input type="checkbox"/>	sp_vs	Q13153-2	Isoform 2 of Q13153 - Homo sapiens (Human) [PAK1]...	87 8e-17
<input type="checkbox"/>	sp	Q05655	KPCD_HUMAN Protein kinase C delta type (EC 2.7.11.13) ...	87 1e-16
<input type="checkbox"/>	sp	Q00526	CDK3_HUMAN Cell division protein kinase 3 (EC 2.7.11.2...	87 1e-16
<input type="checkbox"/>	tr	Q5JPB0	_HUMAN Putative uncharacterized protein DKFZp434B079 [D...	87 1e-16
<input type="checkbox"/>	tr	Q5H9T1	_HUMAN Putative uncharacterized protein DKFZp686D06121 ...	87 1e-16
<input type="checkbox"/>	sp	Q96L34	MARK4_HUMAN MAP/microtubule affinity-regulating kinase...	87 1e-16
<input type="checkbox"/>	sp	Q9UQB9	AURKC_HUMAN Serine/threonine-protein kinase 13 (EC 2.7...	87 1e-16
<input type="checkbox"/>	sp_vs	Q96L34-2	Isoform 2 of Q96L34 - Homo sapiens (Human) [MARK4...	87 1e-16
<input type="checkbox"/>	sp	P17252	KPCA_HUMAN Protein kinase C alpha type (EC 2.7.11.13) ...	86 2e-16
<input type="checkbox"/>	tr	Q2TSD3	_HUMAN Aging-associated gene 6 protein [Homo sapiens (H...	86 2e-16
<input type="checkbox"/>	tr	Q5TSB4	_HUMAN Serine/threonine kinase 24 (STE20 homolog, yeast...	86 2e-16
<input type="checkbox"/>	sp	Q14965	STK6_HUMAN Serine/threonine-protein kinase 6 (EC 2.7.1...	86 3e-16
<input type="checkbox"/>	sp	Q13188	STK3_HUMAN Serine/threonine-protein kinase 3 (EC 2.7.1...	85 4e-16
<input type="checkbox"/>	sp	Q95747	OXSRL_HUMAN Serine/threonine-protein kinase OSR1 (EC 2...	85 4e-16
<input type="checkbox"/>	sp	Q60285	NUAK1_HUMAN NUA family SNF1-like kinase 1 (EC 2.7.11....	85 4e-16
<input type="checkbox"/>	tr	Q6ZNR9	_HUMAN CDNA FLJ27266 fis, clone TMS00356, highly simila...	85 4e-16
<input type="checkbox"/>	tr	A7MD39	_HUMAN NUA family, SNF1-like kinase, 1 (NUAK family, S...	85 4e-16
<input type="checkbox"/>	sp	Q00506	STK25_HUMAN Serine/threonine-protein kinase 25 (EC 2.7...	84 6e-16
<input type="checkbox"/>	sp	Q9HC98	NEK6_HUMAN Serine/threonine-protein kinase Nek6 (EC 2....	84 6e-16
<input type="checkbox"/>	sp	P06493	CDC2_HUMAN Cell division control protein 2 homolog (EC...	84 6e-16
<input type="checkbox"/>	tr	Q96BA2	_HUMAN STK25 protein [Homo sapiens (Human)]	84 6e-16
<input type="checkbox"/>	tr	Q6FG86	_HUMAN NEK6 protein (Fragment) [NEK6] [Homo sapiens (Hu...	84 6e-16
<input type="checkbox"/>	tr	Q5VZ16	_HUMAN NIMA (Never in mitosis gene a)-related kinase 6 ...	84 6e-16
<input type="checkbox"/>	tr	Q5VZ09	_HUMAN NIMA (Never in mitosis gene a)-related kinase 6 ...	84 6e-16
<input type="checkbox"/>	sp	Q59H18	TNI3K_HUMAN Serine/threonine-protein kinase TNI3K (EC...	84 8e-16



<input type="checkbox"/>	tr	Q6DLZ0	_HUMAN Aurora/Ipl1-related kinase 3 transcript variant ...	84	8e-16
<input type="checkbox"/>	tr	Q6AZY8	_HUMAN AURKC protein (Aurora kinase C, isoform CRA_a) [...	84	8e-16
<input type="checkbox"/>	tr	Q5Y191	_HUMAN Aurora-C [AURKC] [Homo sapiens (Human)]	84	8e-16
<input type="checkbox"/>	tr	Q3B785	_HUMAN CDC2 protein [CDC2] [Homo sapiens (Human)]	84	8e-16
<input type="checkbox"/>	tr	Q17RNO	_HUMAN TNNI3 interacting kinase [TNNI3K] [Homo sapiens ...	84	8e-16
<input type="checkbox"/>	sp_vs	Q9UQB9-2	Isoform 2 of Q9UQB9 - Homo sapiens (Human) [AURKC...	84	8e-16
<input type="checkbox"/>	sp_vs	Q59H18-2	Isoform 2 of Q59H18 - Homo sapiens (Human) [TNNI3...	84	8e-16
<input type="checkbox"/>	sp	Q94779	CNTN5_HUMAN Contactin-5 precursor (Neural recognition ...	84	1e-15
<input type="checkbox"/>	tr	Q49AF3	_HUMAN CNTN5 protein [CNTN5] [Homo sapiens (Human)]	84	1e-15
<input type="checkbox"/>	tr	A1L4P0	_HUMAN CNTN5 protein [CNTN5] [Homo sapiens (Human)]	84	1e-15
<input type="checkbox"/>	sp_vs	Q94779-2	Isoform 2 of Q94779 - Homo sapiens (Human) [CNTN5...	84	1e-15
<input type="checkbox"/>	sp_vs	Q9BYT3-2	Isoform 2 of Q9BYT3 - Homo sapiens (Human) [STK33...	84	1e-15
<input type="checkbox"/>	sp	Q56UN5	YSK4_HUMAN SPS1/STE20-related protein kinase YSK4 (EC ...	83	1e-15
<input type="checkbox"/>	sp	Q14680	MELK_HUMAN Maternal embryonic leucine zipper kinase (E...	83	1e-15
<input type="checkbox"/>	tr	Q5T263	_HUMAN Maternal embryonic leucine zipper kinase (Matern...	83	1e-15
<input type="checkbox"/>	tr	Q53GX0	_HUMAN Maternal embryonic leucine zipper kinase variant...	83	1e-15
<input type="checkbox"/>	sp_vs	Q56UN5-3	Isoform 3 of Q56UN5 - Homo sapiens (Human) [YSK4]...	83	1e-15
<input type="checkbox"/>	sp_vs	Q56UN5-5	Isoform 5 of Q56UN5 - Homo sapiens (Human) [YSK4]...	83	1e-15
<input type="checkbox"/>	sp	Q00534	CDK6_HUMAN Cell division protein kinase 6 (EC 2.7.11.2...	83	2e-15
<input type="checkbox"/>	tr	Q5H9N4	_HUMAN Putative uncharacterized protein DKFZp686L20222 ...	83	2e-15
<input type="checkbox"/>	tr	A4D1G0	_HUMAN Cyclin-dependent kinase 6 (HCG19542) [CDK6] [Hom...	83	2e-15
<input type="checkbox"/>	sp	Q96GD4	AURKB_HUMAN Serine/threonine-protein kinase 12 (EC 2.7...	82	2e-15
<input type="checkbox"/>	tr	Q6IAR3	_HUMAN NEK6 protein [NEK6] [Homo sapiens (Human)]	82	2e-15
<input type="checkbox"/>	tr	A3KFX0	_HUMAN Aurora kinase A [AURKA] [Homo sapiens (Human)]	82	2e-15
<input type="checkbox"/>	tr	A2ABM8	_HUMAN Discoidin domain receptor family, member 1 (Frag...	82	2e-15
<input type="checkbox"/>	tr	A2ABL3	_HUMAN Discoidin domain receptor family, member 1 (Frag...	82	2e-15
<input type="checkbox"/>	sp	Q6P5Z2	PKN3_HUMAN Serine/threonine-protein kinase N3 (EC 2.7....	82	3e-15
<input type="checkbox"/>	tr	Q86VS1	_HUMAN Protein kinase, AMP-activated, alpha 1 catalytic...	82	3e-15
<input type="checkbox"/>	tr	Q7L3H5	_HUMAN LIM domain kinase 2 (LIM domain kinase 2, isofor...	82	3e-15
<input type="checkbox"/>	sp	P57059	SN1L1_HUMAN Serine/threonine-protein kinase SNF1-like ...	82	4e-15
<input type="checkbox"/>	sp	Q6ZN16	M3K15_HUMAN Mitogen-activated protein kinase kinase ki...	82	4e-15
<input type="checkbox"/>	sp	Q13131	AAPK1_HUMAN 5'-AMP-activated protein kinase catalytic ...	82	4e-15
<input type="checkbox"/>	sp_vs	Q6ZN16-2	Isoform 2 of Q6ZN16 - Homo sapiens (Human) [MAP3K...	82	4e-15
<input type="checkbox"/>	sp_vs	Q6ZN16-3	Isoform 3 of Q6ZN16 - Homo sapiens (Human) [MAP3K...	82	4e-15
<input type="checkbox"/>	sp	Q16512	PKN1_HUMAN Serine/threonine-protein kinase N1 (EC 2.7....	81	5e-15
<input type="checkbox"/>	sp	Q13177	PAK2_HUMAN Serine/threonine-protein kinase PAK 2 (EC 2...	81	5e-15
<input type="checkbox"/>	sp_vs	Q9UPZ9-2	Isoform 2 of Q9UPZ9 - Homo sapiens (Human) [ICK] ...	81	5e-15
<input type="checkbox"/>	sp	Q9H4B4	PLK3_HUMAN Serine/threonine-protein kinase PLK3 (EC 2....	81	7e-15
<input type="checkbox"/>	sp	Q8NG66	NEK11_HUMAN Serine/threonine-protein kinase Nek11 (EC ...	81	7e-15
<input type="checkbox"/>	sp	Q9UK32	KS6A6_HUMAN Ribosomal protein S6 kinase alpha-6 (EC 2....	81	7e-15
<input type="checkbox"/>	sp	Q9NWZ3	IRAK4_HUMAN Interleukin-1 receptor-associated kinase 4...	81	7e-15
<input type="checkbox"/>	sp	Q9UPZ9	ICK_HUMAN Serine/threonine-protein kinase ICK (EC 2.7....	81	7e-15
<input type="checkbox"/>	sp	Q9P232	CNTN3_HUMAN Contactin-3 precursor (Brain-derived immun...	81	7e-15
<input type="checkbox"/>	tr	Q69FE3	_HUMAN Interleukin-1 receptor-associated kinase 4 varia...	81	7e-15
<input type="checkbox"/>	tr	Q5JR99	_HUMAN Polo-like kinase 3 (Drosophila) [PLK3] [Homo sap...	81	7e-15
<input type="checkbox"/>	tr	Q75271	_HUMAN R31237_1, (Fragment) [Homo sapiens (Human)]	81	7e-15
<input type="checkbox"/>	tr	A7MD41	_HUMAN Intestinal cell (MAK-like) kinase (Intestinal ce...	81	7e-15
<input type="checkbox"/>	tr	A6NKA6	_HUMAN Uncharacterized protein CDKL5 [CDKL5] [Homo sapi...	81	7e-15
<input type="checkbox"/>	tr	A6NHD7	_HUMAN Uncharacterized protein NEK11 [NEK11] [Homo sapi...	81	7e-15
<input type="checkbox"/>	sp_vs	Q8NG66-2	Isoform 2 of Q8NG66 - Homo sapiens (Human) [NEK11...	81	7e-15
<input type="checkbox"/>	sp_vs	Q8NG66-3	Isoform 3 of Q8NG66 - Homo sapiens (Human) [NEK11...	81	7e-15
<input type="checkbox"/>	sp	Q13153	PAK1_HUMAN Serine/threonine-protein kinase PAK 1 (EC 2...	80	9e-15
<input type="checkbox"/>	sp	Q99683	M3K5_HUMAN Mitogen-activated protein kinase kinase kin...	80	9e-15
<input type="checkbox"/>	tr	Q6ZNI2	_HUMAN CDNA FLJ16039 fis, clone ADRGL2001554, weakly si...	80	9e-15
<input type="checkbox"/>	tr	Q59GL6	_HUMAN Mitogen-activated protein kinase kinase kinase 5...	80	9e-15
<input type="checkbox"/>	tr	A6NKM9	_HUMAN Uncharacterized protein MAP3K5 (Fragment) [MAP3K...	80	9e-15
<input type="checkbox"/>	tr	A6NIA0	_HUMAN Uncharacterized protein MAP3K5 [MAP3K5] [Homo sa...	80	9e-15
<input type="checkbox"/>	sp	Q9BYT3	STK33_HUMAN Serine/threonine-protein kinase 33 (EC 2.7...	80	1e-14
<input type="checkbox"/>	sp	Q9NYY3	PLK2_HUMAN Serine/threonine-protein kinase PLK2 (EC 2....	80	1e-14
<input type="checkbox"/>	sp	Q8IVH8	M4K3_HUMAN Mitogen-activated protein kinase kinase kin...	80	1e-14
<input type="checkbox"/>	sp	P54646	AAPK2_HUMAN 5'-AMP-activated protein kinase catalytic ...	80	1e-14
<input type="checkbox"/>	tr	Q92626	_HUMAN Peroxidase homolog (Melanoma-associated antigen...	80	1e-14
<input type="checkbox"/>	tr	Q8N7M6	_HUMAN CDNA FLJ40844 fis, clone TRACH2014356, highly si...	80	1e-14
<input type="checkbox"/>	tr	Q6IQ39	_HUMAN MAP4K3 protein (Mitogen-activated protein kinase...	80	1e-14
<input type="checkbox"/>	tr	Q69FE1	_HUMAN Interleukin-1 receptor-associated kinase 4 short...	80	1e-14
<input type="checkbox"/>	tr	Q4KMG2	_HUMAN PXDN protein (Fragment) [PXDN] [Homo sapiens (Hu...	80	1e-14

<input type="checkbox"/>	sp_vs	Q8IVH8-3	Isoform 3 of Q8IVH8 - Homo sapiens (Human) [MAP4K...	80	1e-14
<input type="checkbox"/>	sp	Q9UKE5	TNIK_HUMAN TRAF2 and NCK-interacting protein kinase (E...	80	2e-14
<input type="checkbox"/>	sp	P20794	MAK_HUMAN Serine/threonine-protein kinase MAK (EC 2.7....	80	2e-14
<input type="checkbox"/>	sp	P57058	HUNK_HUMAN Hormonally up-regulated neu tumor-associate...	80	2e-14
<input type="checkbox"/>	sp	O76039	CDKL5_HUMAN Cyclin-dependent kinase-like 5 (EC 2.7.11....	80	2e-14
<input type="checkbox"/>	sp	Q92772	CDKL2_HUMAN Cyclin-dependent kinase-like 2 (EC 2.7.11....	80	2e-14
<input type="checkbox"/>	tr	Q8IXN4	_HUMAN MAK protein [Homo sapiens (Human)]	80	2e-14
<input type="checkbox"/>	tr	Q547D0	_HUMAN Male germ cell-associated kinase (Male germ cell...	80	2e-14
<input type="checkbox"/>	tr	A7E2A3	_HUMAN TRAF2 and NCK interacting kinase (TRAF2 and NCK ...	80	2e-14
<input type="checkbox"/>	tr	A0MZP5	_HUMAN AMP-activated alpha 2 subunit [PRKAA2] [Homo sap...	80	2e-14
<input type="checkbox"/>	sp_vs	Q9UKE5-2	Isoform 2 of Q9UKE5 - Homo sapiens (Human) [TNIK]...	80	2e-14
<input type="checkbox"/>	sp_vs	Q9UKE5-3	Isoform 3 of Q9UKE5 - Homo sapiens (Human) [TNIK]...	80	2e-14
<input type="checkbox"/>	sp_vs	Q9UKE5-4	Isoform 4 of Q9UKE5 - Homo sapiens (Human) [TNIK]...	80	2e-14
<input type="checkbox"/>	sp_vs	Q9UKE5-5	Isoform 5 of Q9UKE5 - Homo sapiens (Human) [TNIK]...	80	2e-14
<input type="checkbox"/>	sp_vs	Q9UKE5-6	Isoform 6 of Q9UKE5 - Homo sapiens (Human) [TNIK]...	80	2e-14
<input type="checkbox"/>	sp_vs	Q9UKE5-7	Isoform 7 of Q9UKE5 - Homo sapiens (Human) [TNIK]...	80	2e-14
<input type="checkbox"/>	sp_vs	Q9UKE5-8	Isoform 8 of Q9UKE5 - Homo sapiens (Human) [TNIK]...	80	2e-14
<input type="checkbox"/>	sp	Q00537	PCTK2_HUMAN Serine/threonine-protein kinase PCTAIRE-2 ...	79	2e-14
<input type="checkbox"/>	sp	Q8TD19	NEK9_HUMAN Serine/threonine-protein kinase Nek9 (EC 2....	79	2e-14
<input type="checkbox"/>	sp	Q8IWW2	CNTN4_HUMAN Contactin-4 precursor (Brain-derived immun...	79	2e-14
<input type="checkbox"/>	tr	Q59FN2	_HUMAN P21-activated kinase 2 variant (Fragment) [Homo ...	79	2e-14
<input type="checkbox"/>	sp_vs	Q8IWW2-3	Isoform 3 of Q8IWW2 - Homo sapiens (Human) [CNTN4...	79	2e-14
<input type="checkbox"/>	sp	Q8IYT8	ULK2_HUMAN Serine/threonine-protein kinase ULK2 (EC 2....	79	3e-14
<input type="checkbox"/>	sp	Q8IVT5	KSR1_HUMAN Kinase suppressor of Ras 1 [KSR1] [Homo sap...	79	3e-14
<input type="checkbox"/>	sp	Q4KMG0	CDON_HUMAN Cell adhesion molecule-related/down-regulat...	79	3e-14
<input type="checkbox"/>	tr	Q8NC04	_HUMAN CDNA FLJ90626 fis, clone PLACE1003135, weakly si...	79	3e-14
<input type="checkbox"/>	tr	Q15523	_HUMAN Serine/threonine protein kinase [Homo sapiens (H...	79	3e-14
<input type="checkbox"/>	sp_vs	Q4KMG0-2	Isoform 2 of Q4KMG0 - Homo sapiens (Human) [CDON]...	79	3e-14
<input type="checkbox"/>	sp_vs	Q8IVT5-2	Isoform 2 of Q8IVT5 - Homo sapiens (Human) [KSR1]...	79	3e-14
<input type="checkbox"/>	sp_vs	Q8IVT5-3	Isoform 3 of Q8IVT5 - Homo sapiens (Human) [KSR1]...	79	3e-14
<input type="checkbox"/>	sp	Q15759	MK11_HUMAN Mitogen-activated protein kinase 11 (EC 2.7...	79	4e-14
<input type="checkbox"/>	sp	P51841	GUC2F_HUMAN Retinal guanylyl cyclase 2 precursor (EC 4...	79	4e-14
<input type="checkbox"/>	tr	Q86VU3	_HUMAN MAP4K2 protein (Mitogen-activated protein kinase...	79	4e-14
<input type="checkbox"/>	sp_vs	Q96S53-2	Isoform 2 of Q96S53 - Homo sapiens (Human) [TESK2...	79	4e-14
<input type="checkbox"/>	sp	Q8N4C8	MINK1_HUMAN Misshapen-like kinase 1 (EC 2.7.11.1) (Mit...	78	5e-14
<input type="checkbox"/>	sp	Q92918	M4K1_HUMAN Mitogen-activated protein kinase kinase kin...	78	5e-14
<input type="checkbox"/>	sp	Q8IVW4	CDKL3_HUMAN Cyclin-dependent kinase-like 3 (EC 2.7.11....	78	5e-14
<input type="checkbox"/>	tr	Q5U8Z0	_HUMAN Misshapen/NIKs-related kinase isoform beta [MINK...	78	5e-14
<input type="checkbox"/>	tr	Q5JPK7	_HUMAN Ribosomal protein S6 kinase, 90kDa, polypeptide ...	78	5e-14
<input type="checkbox"/>	sp_vs	Q8IVW4-2	Isoform 2 of Q8IVW4 - Homo sapiens (Human) [CDKL3...	78	5e-14
<input type="checkbox"/>	sp_vs	Q8IVH8-2	Isoform 2 of Q8IVH8 - Homo sapiens (Human) [MAP4K...	78	5e-14
<input type="checkbox"/>	sp_vs	Q8N4C8-2	Isoform 1 of Q8N4C8 - Homo sapiens (Human) [MINK1...	78	5e-14
<input type="checkbox"/>	sp_vs	Q8N4C8-3	Isoform 2 of Q8N4C8 - Homo sapiens (Human) [MINK1...	78	5e-14
<input type="checkbox"/>	sp_vs	Q59H18-4	Isoform 4 of Q59H18 - Homo sapiens (Human) [TNIN3...	78	5e-14
<input type="checkbox"/>	sp	O75914	PAK3_HUMAN Serine/threonine-protein kinase PAK 3 (EC 2...	78	6e-14
<input type="checkbox"/>	sp	O95819	M4K4_HUMAN Mitogen-activated protein kinase kinase kin...	78	6e-14
<input type="checkbox"/>	tr	Q6ZMM4	_HUMAN CDNA FLJ16821 fis, clone TRACH3021066, highly si...	78	6e-14
<input type="checkbox"/>	tr	Q59ED6	_HUMAN Polo-like kinase 3 variant (Fragment) [Homo sapi...	78	6e-14
<input type="checkbox"/>	sp_vs	O95819-2	Isoform 2 of O95819 - Homo sapiens (Human) [MAP4K...	78	6e-14
<input type="checkbox"/>	sp_vs	O95819-3	Isoform 3 of O95819 - Homo sapiens (Human) [MAP4K...	78	6e-14
<input type="checkbox"/>	sp_vs	O95819-4	Isoform 4 of O95819 - Homo sapiens (Human) [MAP4K...	78	6e-14
<input type="checkbox"/>	sp_vs	O95819-5	Isoform 5 of O95819 - Homo sapiens (Human) [MAP4K...	78	6e-14
<input type="checkbox"/>	sp_vs	O75914-2	Isoform 2 of O75914 - Homo sapiens (Human) [PAK3]...	78	6e-14
<input type="checkbox"/>	sp	O75385	ULK1_HUMAN Serine/threonine-protein kinase ULK1 (EC 2....	77	8e-14
<input type="checkbox"/>	sp	Q96PF2	TSSK2_HUMAN Testis-specific serine/threonine-protein k...	77	8e-14
<input type="checkbox"/>	sp	Q7L7X3	TAOK1_HUMAN Serine/threonine-protein kinase TAO1 (EC 2...	77	8e-14
<input type="checkbox"/>	sp	Q12851	M4K2_HUMAN Mitogen-activated protein kinase kinase kin...	77	8e-14
<input type="checkbox"/>	sp	P05129	KPCG_HUMAN Protein kinase C gamma type (EC 2.7.11.13) ...	77	8e-14
<input type="checkbox"/>	tr	Q6A1A2	_HUMAN PDPK2 protein [PDPK2] [Homo sapiens (Human)]	77	8e-14
<input type="checkbox"/>	tr	A2RUT8	_HUMAN TAO kinase 1 (TAO kinase 1, isoform CRA_a) [TAOK...	77	8e-14
<input type="checkbox"/>	tr	A0ZT99	_HUMAN Testis-specific serine kinase 2 (HCG1641087) [TS...	77	8e-14
<input type="checkbox"/>	sp	P53350	PLK1_HUMAN Serine/threonine-protein kinase PLK1 (EC 2....	77	1e-13
<input type="checkbox"/>	sp	Q14012	KCC1A_HUMAN Calcium/calmodulin-dependent protein kinas...	77	1e-13
<input type="checkbox"/>	sp_vs	Q96RW7-3	Isoform 3 of Q96RW7 - Homo sapiens (Human) [HMCN1...	77	1e-13
<input type="checkbox"/>	sp	Q6PHR2	ULK3_HUMAN Serine/threonine-protein kinase ULK3 (EC 2....	77	1e-13
<input type="checkbox"/>	sp	O15530	PDPK1_HUMAN 3-phosphoinositide-dependent protein kinas...	77	1e-13

<input type="checkbox"/>	sp	Q00536	PCTK1_HUMAN Serine/threonine-protein kinase PCTAIRE-1 ...	77	1e-13
<input type="checkbox"/>	sp	Q16539	MK14_HUMAN Mitogen-activated protein kinase 14 (EC 2.7...	77	1e-13
<input type="checkbox"/>	tr	Q9UPJ8	_HUMAN PkB-like (Fragment) [PkB-like 1] [Homo sapiens (...]	77	1e-13
<input type="checkbox"/>	tr	Q9BRL4	_HUMAN PCTK1 protein [PCTK1] [Homo sapiens (Human)]	77	1e-13
<input type="checkbox"/>	tr	Q96GA5	_HUMAN PCTK1 protein (Fragment) [PCTK1] [Homo sapiens (...]	77	1e-13
<input type="checkbox"/>	tr	Q6FI20	_HUMAN PDPK1 protein [PDPK1] [Homo sapiens (Human)]	77	1e-13
<input type="checkbox"/>	tr	Q59EH6	_HUMAN 3-phosphoinositide dependent protein kinase-1 va...	77	1e-13
<input type="checkbox"/>	tr	A6P3A7	_HUMAN Maternal embryonic leucine zipper kinase v2 [MEL...	77	1e-13
<input type="checkbox"/>	sp_vs	P11362-15	Isoform 16 of P11362 - Homo sapiens (Human) [FGF...	77	1e-13
<input type="checkbox"/>	sp_vs	Q16539-3	Isoform Mxi2 of Q16539 - Homo sapiens (Human) [MA...	77	1e-13
<input type="checkbox"/>	sp_vs	Q16539-4	Isoform Ezip of Q16539 - Homo sapiens (Human) [MA...	77	1e-13
<input type="checkbox"/>	sp_vs	Q15530-2	Isoform 2 of Q15530 - Homo sapiens (Human) [PDPK1...	77	1e-13
<input type="checkbox"/>	sp	Q9HCK4	ROBO2_HUMAN Roundabout homolog 2 precursor [ROBO2] [Ho...	76	2e-13
<input type="checkbox"/>	sp	Q9UQ07	MOK_HUMAN MAPK/MAK/MRK overlapping kinase (EC 2.7.11.2...	76	2e-13
<input type="checkbox"/>	sp	Q5S007	LRRK2_HUMAN Leucine-rich repeat serine/threonine-prote...	76	2e-13
<input type="checkbox"/>	tr	Q19AB5	_HUMAN ROBO2 isoform a [Homo sapiens (Human)]	76	2e-13
<input type="checkbox"/>	tr	Q19AB4	_HUMAN ROBO2 isoform b (Roundabout, axon guidance recep...	76	2e-13
<input type="checkbox"/>	tr	Q17RV3	_HUMAN Leucine-rich repeat kinase 2 [LRRK2] [Homo sapie...	76	2e-13
<input type="checkbox"/>	tr	A6NJU2	_HUMAN Uncharacterized protein LRRK2 [LRRK2] [Homo sapi...	76	2e-13
<input type="checkbox"/>	tr	A6NC64	_HUMAN Uncharacterized protein SNF1LK [SNF1LK] [Homo sa...	76	2e-13
<input type="checkbox"/>	sp_vs	Q9UQ07-2	Isoform 2 of Q9UQ07 - Homo sapiens (Human) [RAGE]...	76	2e-13
<input type="checkbox"/>	sp_vs	Q9HCK4-2	Isoform 2 of Q9HCK4 - Homo sapiens (Human) [ROBO2...	76	2e-13
<input type="checkbox"/>	sp	Q8WZ42	TITIN_HUMAN Titin (EC 2.7.11.1) (Connectin) (Rhabdomyo...	76	2e-13
<input type="checkbox"/>	sp	Q9Y2K2	QSK_HUMAN Serine/threonine-protein kinase QSK (EC 2.7....	76	2e-13
<input type="checkbox"/>	sp	Q00535	CDK5_HUMAN Cell division protein kinase 5 (EC 2.7.11.2...	76	2e-13
<input type="checkbox"/>	tr	Q9NWX4	_HUMAN CDNA FLJ20549 fis, clone KAT11561 [Homo sapiens ...]	76	2e-13
<input type="checkbox"/>	tr	A6NI10	_HUMAN Uncharacterized protein ENSP00000364441 [Homo sa...	76	2e-13
<input type="checkbox"/>	tr	A1A5A8	_HUMAN KIAA0999 protein [KIAA0999] [Homo sapiens (Human)]	76	2e-13
<input type="checkbox"/>	sp_vs	Q9Y2K2-3	Isoform 3 of Q9Y2K2 - Homo sapiens (Human) [QSK] ...	76	2e-13
<input type="checkbox"/>	sp_vs	Q8WZ42-2	Isoform 2 of Q8WZ42 - Homo sapiens (Human) [TTN] ...	76	2e-13
<input type="checkbox"/>	sp_vs	Q8WZ42-4	Isoform 4 of Q8WZ42 - Homo sapiens (Human) [TTN] ...	76	2e-13
<input type="checkbox"/>	sp_vs	Q8WZ42-5	Isoform 5 of Q8WZ42 - Homo sapiens (Human) [TTN] ...	76	2e-13
<input type="checkbox"/>	sp_vs	Q8WZ42-7	Isoform 7 of Q8WZ42 - Homo sapiens (Human) [TTN] ...	76	2e-13
<input type="checkbox"/>	sp_vs	Q8WZ42-8	Isoform 8 of Q8WZ42 - Homo sapiens (Human) [TTN] ...	76	2e-13
<input type="checkbox"/>	sp	Q9NQU5	PAK6_HUMAN Serine/threonine-protein kinase PAK 6 (EC 2...	75	3e-13
<input type="checkbox"/>	sp	Q7Z2Y5	NRK_HUMAN Nik-related protein kinase (EC 2.7.11.1) [NR...	75	3e-13
<input type="checkbox"/>	sp	Q6VAB6	KSR2_HUMAN Kinase suppressor of Ras 2 (hKSR2) [KSR2] [...]	75	3e-13
<input type="checkbox"/>	sp	P24941	CDK2_HUMAN Cell division protein kinase 2 (EC 2.7.11.2...	75	3e-13
<input type="checkbox"/>	tr	Q59GT1	_HUMAN Conserved helix-loop-helix ubiquitous kinase var...	75	3e-13
<input type="checkbox"/>	tr	Q53HJ9	_HUMAN 3-phosphoinositide dependent protein kinase-1 va...	75	3e-13
<input type="checkbox"/>	tr	A7E2B2	_HUMAN CRKRS protein [CRKRS] [Homo sapiens (Human)]	75	3e-13
<input type="checkbox"/>	sp	Q9P286	PAK7_HUMAN Serine/threonine-protein kinase PAK 7 (EC 2...	75	4e-13
<input type="checkbox"/>	sp	Q8IY84	NIM1_HUMAN Serine/threonine-protein kinase NIM1 (EC 2...	75	4e-13
<input type="checkbox"/>	sp	P51955	NEK2_HUMAN Serine/threonine-protein kinase Nek2 (EC 2...	75	4e-13
<input type="checkbox"/>	sp	O15111	IKKA_HUMAN Inhibitor of nuclear factor kappa-B kinase ...	75	4e-13
<input type="checkbox"/>	sp	P11802	CDK4_HUMAN Cell division protein kinase 4 (EC 2.7.11.2...	75	4e-13
<input type="checkbox"/>	sp	Q9NYV4	CD2L7_HUMAN Cell division cycle 2-related protein kina...	75	4e-13
<input type="checkbox"/>	sp	Q14004	CD2L5_HUMAN Cell division cycle 2-like protein kinase ...	75	4e-13
<input type="checkbox"/>	tr	Q9BVE2	_HUMAN CDC2L5 protein [Homo sapiens (Human)]	75	4e-13
<input type="checkbox"/>	tr	Q8TB93	_HUMAN P21(CDKN1A)-activated kinase 7 [PAK7] [Homo sapi...	75	4e-13
<input type="checkbox"/>	tr	Q6PG61	_HUMAN CDK4 protein (Cyclin-dependent kinase 4, isoform...	75	4e-13
<input type="checkbox"/>	tr	Q562E6	_HUMAN Conserved helix-loop-helix ubiquitous kinase [CH...	75	4e-13
<input type="checkbox"/>	sp_vs	Q14004-2	Isoform 2 of Q14004 - Homo sapiens (Human) [CDC2L...	75	4e-13
<input type="checkbox"/>	sp_vs	Q16539-2	Isoform CSBP1 of Q16539 - Homo sapiens (Human) [M...	75	4e-13
<input type="checkbox"/>	sp_vs	P51955-2	Isoform 2 of P51955 - Homo sapiens (Human) [NEK2]...	75	4e-13
<input type="checkbox"/>	sp_vs	P51955-3	Isoform 3 of P51955 - Homo sapiens (Human) [NEK2]...	75	4e-13
<input type="checkbox"/>	sp	Q9H2K8	TAOK3_HUMAN Serine/threonine-protein kinase TAO3 (EC 2...	75	5e-13
<input type="checkbox"/>	sp	Q9UZE5	ST17A_HUMAN Serine/threonine-protein kinase 17A (EC 2...	75	5e-13
<input type="checkbox"/>	sp	Q07002	PCTK3_HUMAN Serine/threonine-protein kinase PCTAIRE-3 ...	75	5e-13
<input type="checkbox"/>	sp	Q9NZJ5	E2AK3_HUMAN Eukaryotic translation initiation factor 2...	75	5e-13
<input type="checkbox"/>	tr	Q6V3A3	_HUMAN PCTAIRE protein kinase 3 isoform a (PCTAIRE prot...	75	5e-13
<input type="checkbox"/>	tr	Q6V3A2	_HUMAN PCTAIRE protein kinase 3 isoform b (PCTAIRE prot...	75	5e-13
<input type="checkbox"/>	tr	Q6IAW3	_HUMAN CDK5 protein [CDK5] [Homo sapiens (Human)]	75	5e-13
<input type="checkbox"/>	tr	Q68DI6	_HUMAN Putative uncharacterized protein DKFZp781H1925 [...]	75	5e-13
<input type="checkbox"/>	tr	Q59G02	_HUMAN PCTAIRE protein kinase 3 isoform b variant (Frag...	75	5e-13
<input type="checkbox"/>	tr	Q53QY0	_HUMAN Putative uncharacterized protein EIF2AK3 (Fragme...	75	5e-13

<input type="checkbox"/>	tr	A4D1V6	_HUMAN Serine/threonine kinase 17a (Apoptosis-inducing)...	75	5e-13
<input type="checkbox"/>	tr	AOAVI1	_HUMAN Eukaryotic translation initiation factor 2-alpha...	75	5e-13
<input type="checkbox"/>	sp	Q8NEV4	MYO3A_HUMAN Myosin IIIA (EC 2.7.11.1) [MYO3A] [Homo sa...	74	7e-13
<input type="checkbox"/>	sp	Q9UQ52	CNTN6_HUMAN Contactin-6 precursor (Neural recognition ...	74	7e-13
<input type="checkbox"/>	tr	Q9Y6B5	_HUMAN PAK2 [Homo sapiens (Human)]	74	7e-13
<input type="checkbox"/>	tr	Q6ZWT8	_HUMAN CDNA FLJ14395 fis, clone HEMBA1003250, weakly si...	74	7e-13
<input type="checkbox"/>	tr	Q5VXI3	_HUMAN Myosin IIIA [MYO3A] [Homo sapiens (Human)]	74	7e-13
<input type="checkbox"/>	tr	Q0VD65	_HUMAN MYO3A protein [MYO3A] [Homo sapiens (Human)]	74	7e-13
<input type="checkbox"/>	tr	Q05AG9	_HUMAN MYO3A protein [MYO3A] [Homo sapiens (Human)]	74	7e-13
<input type="checkbox"/>	sp	Q15831	STK11_HUMAN Serine/threonine-protein kinase 11 (EC 2.7...	74	9e-13
<input type="checkbox"/>	sp	O00444	PLK4_HUMAN Serine/threonine-protein kinase PLK4 (EC 2...	74	9e-13
<input type="checkbox"/>	sp	P23443	KS6B1_HUMAN Ribosomal protein S6 kinase beta-1 (EC 2.7...	74	9e-13
<input type="checkbox"/>	tr	Q9HBS3	_HUMAN Putative uncharacterized protein [Homo sapiens (...	74	9e-13
<input type="checkbox"/>	tr	Q7Z721	_HUMAN RPS6KB1 protein (Ribosomal protein S6 kinase, 70...	74	9e-13
<input type="checkbox"/>	sp_vs	P23443-2	Isoform Alpha II of P23443 - Homo sapiens (Human)...	74	9e-13
<input type="checkbox"/>	sp	O94856	NFASC_HUMAN Neurofascin precursor [NFASC] [Homo sapien...	74	1e-12
<input type="checkbox"/>	tr	Q9H4D1	_HUMAN Protein kinase [dik] [Homo sapiens (Human)]	74	1e-12
<input type="checkbox"/>	tr	Q2TB16	_HUMAN Receptor-interacting serine-threonine kinase 4 (...	74	1e-12
<input type="checkbox"/>	tr	Q15879	_HUMAN Protein kinase (Fragment) [Homo sapiens (Human)]	74	1e-12
<input type="checkbox"/>	tr	Q149P5	_HUMAN NFASC protein [NFASC] [Homo sapiens (Human)]	74	1e-12
<input type="checkbox"/>	sp_vs	O94856-2	Isoform 2 of O94856 - Homo sapiens (Human) [NFASC...	74	1e-12
<input type="checkbox"/>	sp_vs	O94856-3	Isoform 3 of O94856 - Homo sapiens (Human) [NFASC...	74	1e-12
<input type="checkbox"/>	sp_vs	O94856-4	Isoform 4 of O94856 - Homo sapiens (Human) [NFASC...	74	1e-12
<input type="checkbox"/>	sp_vs	O94856-5	Isoform 5 of O94856 - Homo sapiens (Human) [NFASC...	74	1e-12
<input type="checkbox"/>	sp_vs	O94856-6	Isoform 6 of O94856 - Homo sapiens (Human) [NFASC...	74	1e-12
<input type="checkbox"/>	sp_vs	O94856-7	Isoform 7 of O94856 - Homo sapiens (Human) [NFASC...	74	1e-12
<input type="checkbox"/>	sp_vs	O94856-8	Isoform 8 of O94856 - Homo sapiens (Human) [NFASC...	74	1e-12
<input type="checkbox"/>	sp_vs	O94856-9	Isoform 9 of O94856 - Homo sapiens (Human) [NFASC...	74	1e-12
<input type="checkbox"/>	sp_vs	O94856-10	Isoform 10 of O94856 - Homo sapiens (Human) [NFA...	74	1e-12
<input type="checkbox"/>	sp_vs	O94856-11	Isoform 11 of O94856 - Homo sapiens (Human) [NFA...	74	1e-12
<input type="checkbox"/>	sp_vs	O94856-12	Isoform 12 of O94856 - Homo sapiens (Human) [NFA...	74	1e-12
<input type="checkbox"/>	sp_vs	O94856-13	Isoform 13 of O94856 - Homo sapiens (Human) [NFA...	74	1e-12
<input type="checkbox"/>	sp_vs	P57078-2	Isoform 2 of P57078 - Homo sapiens (Human) [RIPK4...	74	1e-12
<input type="checkbox"/>	sp	O95382	M3K6_HUMAN Mitogen-activated protein kinase kinase kin...	73	1e-12
<input type="checkbox"/>	tr	Q5TI62	_HUMAN Ribosomal protein S6 kinase, 90kDa, polypeptide ...	73	1e-12
<input type="checkbox"/>	tr	Q5SSD4	_HUMAN Mitogen-activated protein kinase kinase kinase 6...	73	1e-12
<input type="checkbox"/>	tr	Q32MQ5	_HUMAN MAP3K6 protein [MAP3K6] [Homo sapiens (Human)]	73	1e-12
<input type="checkbox"/>	sp_vs	O95382-2	Isoform 2 of O95382 - Homo sapiens (Human) [MAP3K...	73	1e-12
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<input type="checkbox"/>	sp_vs	Q56UN5-4	Isoform 4 of Q56UN5 - Homo sapiens (Human) [YSK4]...	73	1e-12
<input type="checkbox"/>	sp	Q9BXA6	TSSK6_HUMAN Testis-specific serine/threonine-protein k...	73	2e-12
<input type="checkbox"/>	sp	Q5MAI5	CDKL4_HUMAN Cyclin-dependent kinase-like 4 (EC 2.7.11...	73	2e-12
<input type="checkbox"/>	tr	Q8NDA2	_HUMAN Hemicentin-2 (Fragment) [DKFZp434P0216] [Homo sa...	73	2e-12
<input type="checkbox"/>	tr	Q2NME9	_HUMAN Cyclin-dependent kinase-like 4 [CDKL4] [Homo sap...	73	2e-12
<input type="checkbox"/>	sp	Q9Y4K4	M4K5_HUMAN Mitogen-activated protein kinase kinase kin...	72	3e-12
<input type="checkbox"/>	tr	Q5VZ10	_HUMAN NIMA (Never in mitosis gene a)-related kinase 6 ...	72	3e-12
<input type="checkbox"/>	tr	Q53GK9	_HUMAN MAPK13 protein variant (Fragment) [Homo sapiens ...	72	3e-12
<input type="checkbox"/>	sp	Q15746	MYLK_HUMAN Myosin light chain kinase, smooth muscle (E...	72	3e-12
<input type="checkbox"/>	sp	P11801	KPSH1_HUMAN Serine/threonine-protein kinase H1 (EC 2.7...	72	3e-12
<input type="checkbox"/>	sp	Q9C098	DCLK3_HUMAN Serine/threonine-protein kinase DCLK3 (EC ...	72	3e-12
<input type="checkbox"/>	sp	Q00532	CDKL1_HUMAN Cyclin-dependent kinase-like 1 (EC 2.7.11...	72	3e-12
<input type="checkbox"/>	tr	Q2M3A4	_HUMAN Cyclin-dependent kinase-like 1 (CDC2-related kin...	72	3e-12
<input type="checkbox"/>	sp_vs	Q15746-2	Isoform 2 of Q15746 - Homo sapiens (Human) [MYLK]...	72	3e-12
<input type="checkbox"/>	sp_vs	Q15746-6	Isoform Del-1790 of Q15746 - Homo sapiens (Human)...	72	3e-12
<input type="checkbox"/>	sp	O15264	MK13_HUMAN Mitogen-activated protein kinase 13 (EC 2.7...	72	4e-12
<input type="checkbox"/>	sp	Q02156	KPCE_HUMAN Protein kinase C epsilon type (EC 2.7.11.13...	72	4e-12
<input type="checkbox"/>	sp	P50750	CDK9_HUMAN Cell division protein kinase 9 (EC 2.7.11.2...	72	4e-12
<input type="checkbox"/>	tr	Q96T11	_HUMAN CDNA FLJ14518 fis, clone NT2RM1000850, weakly si...	72	4e-12
<input type="checkbox"/>	tr	Q6FI46	_HUMAN MAPK13 protein (Mitogen-activated protein kinase...	72	4e-12
<input type="checkbox"/>	tr	Q6FHR4	_HUMAN MAPK13 protein (Fragment) [MAPK13] [Homo sapiens...	72	4e-12
<input type="checkbox"/>	tr	A6YR18	_HUMAN Polarization-related protein LKB1 [Homo sapiens ...	72	4e-12
<input type="checkbox"/>	sp_vs	P50750-2	Isoform 2 of P50750 - Homo sapiens (Human) [CDK9]...	72	4e-12
<input type="checkbox"/>	sp	Q92823	NRCAM_HUMAN Neuronal cell adhesion molecule precursor ...	71	6e-12
<input type="checkbox"/>	sp	Q8WXR4	MYO3B_HUMAN Myosin-IIIB (EC 2.7.11.1) [MYO3B] [Homo sa...	71	6e-12
<input type="checkbox"/>	sp	Q8NFD2	ANKK1_HUMAN Ankyrin repeat and protein kinase domain-c...	71	6e-12
<input type="checkbox"/>	tr	Q59FI5	_HUMAN Protein kinase C, alpha variant (Fragment) [Homo...	71	6e-12

<input type="checkbox"/>	tr	Q4KM07	_HUMAN NRCAM protein [NRCAM] [Homo sapiens (Human)]	71	6e-12
<input type="checkbox"/>	tr	Q14CA1	_HUMAN NRCAM protein [NRCAM] [Homo sapiens (Human)]	71	6e-12
<input type="checkbox"/>	tr	Q14BM2	_HUMAN NRCAM protein [NRCAM] [Homo sapiens (Human)]	71	6e-12
<input type="checkbox"/>	tr	A4D0S3	_HUMAN Neuronal cell adhesion molecule (Neuronal cell a...	71	6e-12
<input type="checkbox"/>	sp_vs	Q8WXR4-2	Isoform 2 of Q8WXR4 - Homo sapiens (Human) [MYO3B...	71	6e-12
<input type="checkbox"/>	sp_vs	Q8WXR4-3	Isoform 3 of Q8WXR4 - Homo sapiens (Human) [MYO3B...	71	6e-12
<input type="checkbox"/>	sp_vs	Q8WXR4-4	Isoform 4 of Q8WXR4 - Homo sapiens (Human) [MYO3B...	71	6e-12
<input type="checkbox"/>	sp_vs	Q8WXR4-5	Isoform 5 of Q8WXR4 - Homo sapiens (Human) [MYO3B...	71	6e-12
<input type="checkbox"/>	sp_vs	Q8WXR4-6	Isoform 6 of Q8WXR4 - Homo sapiens (Human) [MYO3B...	71	6e-12
<input type="checkbox"/>	sp_vs	Q8WXR4-7	Isoform 7 of Q8WXR4 - Homo sapiens (Human) [MYO3B...	71	6e-12
<input type="checkbox"/>	sp_vs	Q92823-2	Isoform 2 of Q92823 - Homo sapiens (Human) [NRCAM...	71	6e-12
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<input type="checkbox"/>	sp	Q9UL54	TAOK2_HUMAN Serine/threonine-protein kinase TAO2 (EC 2...	71	7e-12
<input type="checkbox"/>	sp	Q99759	M3K3_HUMAN Mitogen-activated protein kinase kinase kin...	71	7e-12
<input type="checkbox"/>	tr	Q96HN9	_HUMAN Putative uncharacterized protein (Fragment) [Hom...	71	7e-12
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<input type="checkbox"/>	tr	A7MCZ2	_HUMAN TAO kinase 2 (TAO kinase 2, isoform CRA_b) [TAOK...	71	7e-12
<input type="checkbox"/>	tr	A0PJ48	_HUMAN TAOK2 protein (Fragment) [TAOK2] [Homo sapiens (...]	71	7e-12
<input type="checkbox"/>	sp_vs	Q9UL54-2	Isoform 2 of Q9UL54 - Homo sapiens (Human) [TAOK2...	71	7e-12
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<input type="checkbox"/>	sp	Q7Z5N4	SDK1_HUMAN Protein sidekick-1 precursor [SDK1] [Homo s...	70	1e-11
<input type="checkbox"/>	sp	Q5VST9	OBSCN_HUMAN Obscurin (EC 2.7.11.1) (Obscurin-myosin li...	70	1e-11
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<input type="checkbox"/>	tr	Q5VXI1	_HUMAN Myosin IIIA (MYO3A protein) [MYO3A] [Homo sapien...	70	1e-11
<input type="checkbox"/>	tr	A2A391	_HUMAN Obscurin, cytoskeletal calmodulin and titin-inte...	70	1e-11
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<input type="checkbox"/>	sp	Q9BXA7	TSSK1_HUMAN Testis-specific serine/threonine-protein k...	70	1e-11
<input type="checkbox"/>	sp	Q9NRH2	SNRK_HUMAN SNF-related serine/threonine-protein kinase...	70	1e-11
<input type="checkbox"/>	sp	P57078	RIPK4_HUMAN Receptor-interacting serine/threonine-prot...	70	1e-11
<input type="checkbox"/>	sp	Q02246	CNTN2_HUMAN Contactin-2 precursor (Axonin-1) (Axonal g...	70	1e-11
<input type="checkbox"/>	tr	Q8NCE6	_HUMAN CDNA FLJ90299 fis, clone NT2RP2000514, highly si...	70	1e-11
<input type="checkbox"/>	tr	Q59FA7	_HUMAN Serine/threonine protein kinase 11 variant (Frag...	70	1e-11
<input type="checkbox"/>	tr	Q53TX8	_HUMAN Putative uncharacterized protein MAP4K4 (Fragmen...	70	1e-11
<input type="checkbox"/>	tr	A1L3A3	_HUMAN Contactin 2 (Axonal) [CNTN2] [Homo sapiens (Human)]	70	1e-11
<input type="checkbox"/>	tr	A0ZT98	_HUMAN Testis-specific serine kinase 1 [TSSK1] [Homo sa...	70	1e-11
<input type="checkbox"/>	sp	O96013	PAK4_HUMAN Serine/threonine-protein kinase PAK 4 (EC 2...	70	2e-11
<input type="checkbox"/>	sp	P13592	NCA12_HUMAN Neural cell adhesion molecule 1, 120 kDa i...	70	2e-11
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<input type="checkbox"/>	sp	Q9NR99	MXRAS_HUMAN Matrix-remodeling-associated protein 5 pre...	70	2e-11
<input type="checkbox"/>	tr	Q59FL7	_HUMAN Neural cell adhesion molecule 1, 120 kDa isoform...	70	2e-11
<input type="checkbox"/>	sp_vs	P13592-1	Isoform C of P13592 - Homo sapiens (Human) [NCAM1...	70	2e-11
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<input type="checkbox"/>	sp	Q96MS0	ROBO3_HUMAN Roundabout homolog 3 precursor (Roundabout...	69	2e-11
<input type="checkbox"/>	tr	Q68DA2	_HUMAN Putative uncharacterized protein DKFZp781D102 [D...	69	2e-11
<input type="checkbox"/>	tr	Q59GD0	_HUMAN Polo-like kinase variant (Fragment) [Homo sapien...	69	2e-11
<input type="checkbox"/>	tr	Q3KPG9	_HUMAN V-mos Moloney murine sarcoma viral oncogene homo...	69	2e-11
<input type="checkbox"/>	sp_vs	Q8WX93-2	Isoform 2 of Q8WX93 - Homo sapiens (Human) [PALLD...	69	2e-11
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<input type="checkbox"/>	sp	Q9Y243	AKT3_HUMAN RAC-gamma serine/threonine-protein kinase (...]	69	3e-11
<input type="checkbox"/>	tr	Q9BWF9	_HUMAN PCTK3 protein (Fragment) [PCTK3] [Homo sapiens (...]	69	3e-11

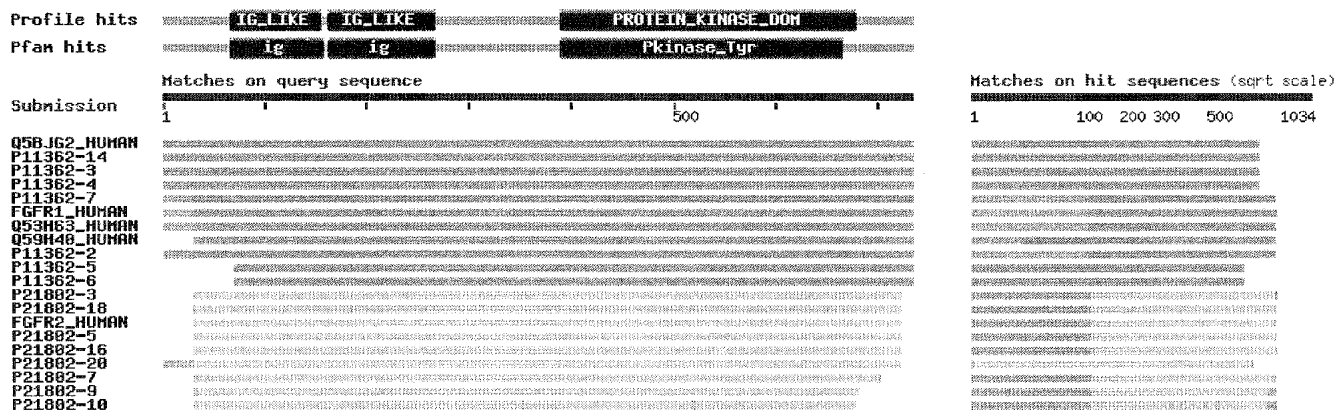
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<input type="checkbox"/>	tr	Q5VTI2	_HUMAN V-akt murine thymoma viral oncogene homolog 3 (P...	69 3e-11
<input type="checkbox"/>	tr	Q5VTI1	_HUMAN V-akt murine thymoma viral oncogene homolog 3 (P...	69 3e-11
<input type="checkbox"/>	tr	Q5SQQ7	_HUMAN Calcium/calmodulin-dependent protein kinase ID (...	69 3e-11
<input type="checkbox"/>	tr	Q56A86	_HUMAN AKT3 protein (Fragment) [AKT3] [Homo sapiens (Hu...	69 3e-11
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<input type="checkbox"/>	sp_vs	Q8WX93-4	Isoform 4 of Q8WX93 - Homo sapiens (Human) [PALLD...	69 3e-11
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<input type="checkbox"/>	sp	Q9Y2U5	M3K2_HUMAN Mitogen-activated protein kinase kinase kin...	69 4e-11
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<input type="checkbox"/>	sp	Q96NX5	KCC1G_HUMAN Calcium/calmodulin-dependent protein kinas...	68 5e-11
<input type="checkbox"/>	sp	Q8TDC3	BRSK1_HUMAN BR serine/threonine-protein kinase 1 (EC 2...	68 5e-11
<input type="checkbox"/>	tr	Q86VY5	_HUMAN MYO3A protein [MYO3A] [Homo sapiens (Human)]	68 5e-11
<input type="checkbox"/>	tr	Q69YJ3	_HUMAN Putative uncharacterized protein DKFZp762L185 (F...	68 5e-11
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<input type="checkbox"/>	sp_vs	Q96NX5-2	Isoform 2 of Q96NX5 - Homo sapiens (Human) [CAMK1...	68 5e-11
<input type="checkbox"/>	sp_vs	Q15746-3	Isoform 3A of Q15746 - Homo sapiens (Human) [MYLK...	68 5e-11
<input type="checkbox"/>	sp_vs	Q15746-4	Isoform 3B of Q15746 - Homo sapiens (Human) [MYLK...	68 5e-11
<input type="checkbox"/>	sp	Q9UBES	NLK_HUMAN Serine/threonine kinase NLK (EC 2.7.11.24) (...	68 6e-11
<input type="checkbox"/>	sp	Q9H1R3	MYLK2_HUMAN Myosin light chain kinase 2, skeletal/card...	68 6e-11
<input type="checkbox"/>	sp	Q96JA1	LRIG1_HUMAN Leucine-rich repeats and immunoglobulin-li...	68 6e-11
<input type="checkbox"/>	sp	Q96QS6	KPSH2_HUMAN Serine/threonine-protein kinase H2 (EC 2.7...	68 6e-11
<input type="checkbox"/>	sp	P14619	KGP1B_HUMAN cGMP-dependent protein kinase 1, beta isoz...	68 6e-11
<input type="checkbox"/>	sp	Q13976	KGP1A_HUMAN cGMP-dependent protein kinase 1, alpha iso...	68 6e-11
<input type="checkbox"/>	sp	P19525	E2AK2_HUMAN Interferon-induced, double-stranded RNA-ac...	68 6e-11
<input type="checkbox"/>	tr	Q9BXC3	_HUMAN Serine/threonine protein kinase MST4a (Mst3 and ...	68 6e-11
<input type="checkbox"/>	tr	Q8IW76	_HUMAN EIF2AK2 protein (Fragment) [EIF2AK2] [Homo sapie...	68 6e-11
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<input type="checkbox"/>	tr	Q6E0B2	_HUMAN Small intestine SPAK-like kinase [Homo sapiens (...	68 6e-11
<input type="checkbox"/>	tr	Q5XWD3	_HUMAN Leucine-rich repeat protein LRIG1 [LRIG1] [Homo ...	68 6e-11
<input type="checkbox"/>	tr	Q5SQU3	_HUMAN Protein kinase, cGMP-dependent, type I [PRKG1] [...	68 6e-11
<input type="checkbox"/>	sp_vs	P11362-17	Isoform 3 of P11362 - Homo sapiens (Human) [FGFR...	68 6e-11
<input type="checkbox"/>	sp	P37173	TGFR2_HUMAN TGF-beta receptor type-2 precursor (EC 2.7...	67 8e-11
<input type="checkbox"/>	sp	Q9UBF9	MYOTI_HUMAN Myotilin (Titin immunoglobulin domain prot...	67 8e-11
<input type="checkbox"/>	sp	Q13163	MP2K5_HUMAN Dual specificity mitogen-activated protein...	67 8e-11
<input type="checkbox"/>	sp	P53355	DAPK1_HUMAN Death-associated protein kinase 1 (EC 2.7....	67 8e-11
<input type="checkbox"/>	sp	Q12860	CNTN1_HUMAN Contactin-1 precursor (Neural cell surface...	67 8e-11
<input type="checkbox"/>	sp	Q9UQ88	CD2L2_HUMAN PITSLRE serine/threonine-protein kinase CD...	67 8e-11

<input type="checkbox"/>	sp	O00238	BMR1B_HUMAN Bone morphogenetic protein receptor type I...	67	8e-11
<input type="checkbox"/>	tr	Q96CA8	_HUMAN CDC2L2 protein (Fragment) [CDC2L2] [Homo sapiens...	67	8e-11
<input type="checkbox"/>	tr	Q5VTK1	_HUMAN Death-associated protein kinase 1 [DAPK1] [Homo ...	67	8e-11
<input type="checkbox"/>	tr	Q5QPR4	_HUMAN Cell division cycle 2-like 2 (PITSLRE proteins) ...	67	8e-11
<input type="checkbox"/>	tr	Q5QPR3	_HUMAN Cell division cycle 2-like 2 (PITSLRE proteins) ...	67	8e-11
<input type="checkbox"/>	tr	Q59H88	_HUMAN Putative uncharacterized protein (Fragment) [Hom...	67	8e-11
<input type="checkbox"/>	tr	Q53EZ9	_HUMAN Mitogen-activated protein kinase kinase 3 isoform...	67	8e-11
<input type="checkbox"/>	tr	Q4VBY6	_HUMAN CDC2L2 protein (Fragment) [CDC2L2] [Homo sapiens...	67	8e-11
<input type="checkbox"/>	tr	Q2TAJ0	_HUMAN Cell division cycle 2-like 2 (PITSLRE proteins) ...	67	8e-11
<input type="checkbox"/>	tr	Q1W5W0	_HUMAN Death-associated protein kinase 1 (Death-associa...	67	8e-11
<input type="checkbox"/>	tr	Q14CQ7	_HUMAN Death-associated protein kinase 1 [DAPK1] [Homo ...	67	8e-11
<input type="checkbox"/>	tr	Q0VAA6	_HUMAN V-akt murine thymoma viral oncogene homolog 3 (P...	67	8e-11
<input type="checkbox"/>	tr	A3QNQ0	_HUMAN Transforming growth factor beta receptor II (Tra...	67	8e-11
<input type="checkbox"/>	tr	AL14K2	_HUMAN Mitogen-activated protein kinase 8 (Mitogen-acti...	67	8e-11
<input type="checkbox"/>	tr	ALKZ92	_HUMAN Cardiac peroxidase [Homo sapiens (Human)]	67	8e-11
<input type="checkbox"/>	sp_vs	Q9UQ88-2	Isoform SV1 of Q9UQ88 - Homo sapiens (Human) [CDC...	67	8e-11
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<input type="checkbox"/>	sp_vs	P37173-2	Isoform 2 of P37173 - Homo sapiens (Human) [TGFB...	67	8e-11
<input type="checkbox"/>	sp	Q86SG6	NEK8_HUMAN Serine/threonine-protein kinase Nek8 (EC 2....	67	1e-10
<input type="checkbox"/>	sp	P46734	MP2K3_HUMAN Dual specificity mitogen-activated protein...	67	1e-10
<input type="checkbox"/>	sp	Q16659	MK06_HUMAN Mitogen-activated protein kinase 6 (EC 2.7....	67	1e-10
<input type="checkbox"/>	sp	Q13237	KGP2_HUMAN cGMP-dependent protein kinase 2 (EC 2.7.11....	67	1e-10
<input type="checkbox"/>	sp	Q6WRI0	IGS10_HUMAN Immunoglobulin superfamily member 10 precu...	67	1e-10
<input type="checkbox"/>	sp	Q14757	CHK1_HUMAN Serine/threonine-protein kinase Chk1 (EC 2....	67	1e-10
<input type="checkbox"/>	tr	Q6FI23	_HUMAN MAP2K3 protein [MAP2K3] [Homo sapiens (Human)]	67	1e-10
<input type="checkbox"/>	tr	Q6PHG1	_HUMAN MAP2K3 protein (Fragment) [MAP2K3] [Homo sapiens...	67	1e-10
<input type="checkbox"/>	tr	Q68DY3	_HUMAN Putative uncharacterized protein DKFZp686P2031 [...	67	1e-10
<input type="checkbox"/>	tr	A6NIC5	_HUMAN Uncharacterized protein NEK8 [NEK8] [Homo sapien...	67	1e-10
<input type="checkbox"/>	sp_vs	Q8TD08-3	Isoform 3 of Q8TD08 - Homo sapiens (Human) [MAPK1...	67	1e-10
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<input type="checkbox"/>	sp_vs	Q15746-5	Isoform 4 of Q15746 - Homo sapiens (Human) [MYLK]...	67	1e-10
<input type="checkbox"/>	sp	Q8TD08	MK15_HUMAN Mitogen-activated protein kinase 15 (EC 2.7...	67	1e-10
<input type="checkbox"/>	sp	Q9UIK4	DAPK2_HUMAN Death-associated protein kinase 2 (EC 2.7....	67	1e-10
<input type="checkbox"/>	sp	P37023	ACV11_HUMAN Serine/threonine-protein kinase receptor R...	67	1e-10
<input type="checkbox"/>	tr	A6NGA8	_HUMAN Uncharacterized protein ACVRL1 [ACVRL1] [Homo sa...	67	1e-10
<input type="checkbox"/>	sp	P36897	TGFR1_HUMAN TGF-beta receptor type-1 precursor (EC 2.7...	66	2e-10
<input type="checkbox"/>	sp	Q8GYV6	SGK85_HUMAN Uncharacterized serine/threonine-protein k...	66	2e-10
<input type="checkbox"/>	sp	P53779	MK10_HUMAN Mitogen-activated protein kinase 10 (EC 2.7...	66	2e-10
<input type="checkbox"/>	sp	Q9UBS0	KS6B2_HUMAN Ribosomal protein S6 kinase beta-2 (EC 2.7...	66	2e-10
<input type="checkbox"/>	sp	P31749	AKT1_HUMAN RAC-alpha serine/threonine-protein kinase (...	66	2e-10
<input type="checkbox"/>	tr	Q9BRS0	_HUMAN Ribosomal protein S6 kinase, 70kDa, polypeptide ...	66	2e-10
<input type="checkbox"/>	tr	Q6F9H2	_HUMAN Mitogen-activated protein kinase kinase 4 [MAP2K...	66	2e-10
<input type="checkbox"/>	tr	Q6IR47	_HUMAN TGFR1 protein [TGFR1] [Homo sapiens (Human)]	66	2e-10
<input type="checkbox"/>	tr	Q5T7S2	_HUMAN Transforming growth factor, beta receptor I (Act...	66	2e-10
<input type="checkbox"/>	tr	A6NG28	_HUMAN Uncharacterized protein MAPK10 [MAPK10] [Homo sa...	66	2e-10
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<input type="checkbox"/>	sp	Q96RG2	PASK_HUMAN PAS domain-containing serine/threonine-prot...	66	2e-10
<input type="checkbox"/>	sp	P27361	MK03_HUMAN Mitogen-activated protein kinase 3 (EC 2.7....	66	2e-10
<input type="checkbox"/>	sp	P21127	CD2L1_HUMAN PITSLRE serine/threonine-protein kinase CD...	66	2e-10
<input type="checkbox"/>	sp	P31751	AKT2_HUMAN RAC-beta serine/threonine-protein kinase (E...	66	2e-10
<input type="checkbox"/>	tr	Q6P5Y5	_HUMAN CDC2L2 protein (Fragment) [CDC2L2] [Homo sapiens...	66	2e-10
<input type="checkbox"/>	tr	Q6FG83	_HUMAN STK17B protein (Fragment) [STK17B] [Homo sapiens...	66	2e-10
<input type="checkbox"/>	tr	A5VM56	_HUMAN PRKG1 protein [PRKG1] [Homo sapiens (Human)]	66	2e-10
<input type="checkbox"/>	tr	A4VC15	_HUMAN CDC2L1 protein (Fragment) [CDC2L1] [Homo sapiens...	66	2e-10
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<input type="checkbox"/>	sp_vs	P21127-4	Isoform 3 of P21127 - Homo sapiens (Human) [CDC2L...	66	2e-10
<input type="checkbox"/>	sp_vs	P21127-5	Isoform SV4 of P21127 - Homo sapiens (Human) [CDC...	66	2e-10

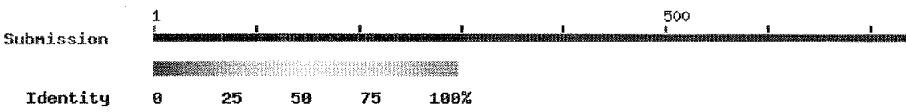
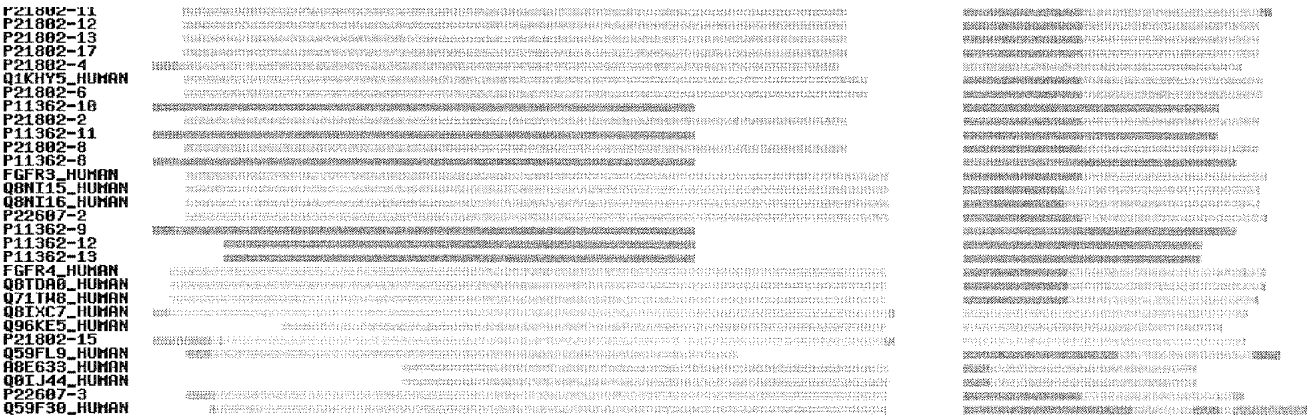
<input type="checkbox"/>	sp_vs P21127-6	Isoform SV5 of P21127 - Homo sapiens (Human) [CDC...	66 2e-10
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<input type="checkbox"/>	sp_vs P21127-9	Isoform SV10 of P21127 - Homo sapiens (Human) [CD...	66 2e-10
<input type="checkbox"/>	sp_vs P21127-10	Isoform SV11 of P21127 - Homo sapiens (Human) [C...	66 2e-10
<input type="checkbox"/>	sp_vs P21127-12	Isoform 7 of P21127 - Homo sapiens (Human) [CDC2...	66 2e-10
<input type="checkbox"/>	sp_vs Q96RG2-2	Isoform 2 of Q96RG2 - Homo sapiens (Human) [PASK]...	66 2e-10
<input type="checkbox"/>	sp_vs O15530-3	Isoform 3 of O15530 - Homo sapiens (Human) [PDPK1...	66 2e-10
<input type="checkbox"/>	sp O43930	PRKY_HUMAN Serine/threonine-protein kinase PRKY (EC 2...	65 3e-10
<input type="checkbox"/>	sp P98160	PGBM_HUMAN Basement membrane-specific heparan sulfate ...	65 3e-10
<input type="checkbox"/>	sp Q38SD2	LRRK1_HUMAN Leucine-rich repeat serine/threonine-prote...	65 3e-10
<input type="checkbox"/>	sp P24723	KPCL_HUMAN Protein kinase C eta type (EC 2.7.11.13) (n...	65 3e-10
<input type="checkbox"/>	sp Q8N5S9	KKCC1_HUMAN Calcium/calmodulin-dependent protein kinas...	65 3e-10
<input type="checkbox"/>	sp Q04771	ACVR1_HUMAN Activin receptor type-1 precursor (EC 2.7...	65 3e-10
<input type="checkbox"/>	tr Q8NE03	_HUMAN Protein kinase C, eta (Protein kinase C, eta, is...	65 3e-10
<input type="checkbox"/>	tr Q5VU27	_HUMAN Heparan sulfate proteoglycan 2 [HSPG2] [Homo sap...	65 3e-10
<input type="checkbox"/>	tr A8CZ58	_HUMAN Extracellular signal-regulated kinase-1 splice v...	65 3e-10
<input type="checkbox"/>	tr A6NDF7	_HUMAN Uncharacterized protein HSPG2 [HSPG2] [Homo sapi...	65 3e-10
<input type="checkbox"/>	tr A6H8V9	_HUMAN LRRK1 protein (Fragment) [LRRK1] [Homo sapiens (...]	65 3e-10
<input type="checkbox"/>	sp_vs Q38SD2-3	Isoform 3 of Q38SD2 - Homo sapiens (Human) [LRRK1...	65 3e-10
<input type="checkbox"/>	sp O94768	ST17B_HUMAN Serine/threonine-protein kinase 17B (EC 2...	65 4e-10
<input type="checkbox"/>	sp C14976	GAK_HUMAN Cyclin G-associated kinase (EC 2.7.11.1) [GA...	65 4e-10
<input type="checkbox"/>	tr Q6FG98	_HUMAN STK17B protein [STK17B] [Homo sapiens (Human)]	65 4e-10
<input type="checkbox"/>	tr Q53QE7	_HUMAN Putative uncharacterized protein STK17B (Serine/...	65 4e-10
<input type="checkbox"/>	sp_vs Q8TD08-2	Isoform 2 of Q8TD08 - Homo sapiens (Human) [MAPK1...	65 4e-10
<input type="checkbox"/>	sp Q496M5	PLK5_HUMAN Serine/threonine-protein kinase PLK5 (EC 2...	65 5e-10
<input type="checkbox"/>	sp Q92859	NEO1_HUMAN Neogenin precursor [NEO1] [Homo sapiens (Hu...	65 5e-10
<input type="checkbox"/>	sp Q6P2M8	KCC1B_HUMAN Calcium/calmodulin-dependent protein kinas...	65 5e-10
<input type="checkbox"/>	sp Q15075	DCLK1_HUMAN Serine/threonine-protein kinase DCLK1 (EC ...	65 5e-10
<input type="checkbox"/>	tr Q5VZZ1	_HUMAN Doublecortin and CaM kinase-like 1 (Doublecortin...	65 5e-10
<input type="checkbox"/>	tr Q5VZZ0	_HUMAN Doublecortin and CaM kinase-like 1 (Doublecortin...	65 5e-10
<input type="checkbox"/>	tr Q5VZY8	_HUMAN Doublecortin and CaM kinase-like 1 [DCAMKL1] [Ho...	65 5e-10
<input type="checkbox"/>	tr Q3MS94	_HUMAN Dominant-negative kinase-deficient Brutons tyros...	65 5e-10
<input type="checkbox"/>	tr A6N135	_HUMAN Uncharacterized protein HSPG2 [HSPG2] [Homo sapi...	65 5e-10
<input type="checkbox"/>	tr A6NHX2	_HUMAN Uncharacterized protein ENSP00000329329 (Fragmen...	65 5e-10
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<input type="checkbox"/>	sp_vs Q496M5-2	Isoform 2 of Q496M5 - Homo sapiens (Human) [PLK5]...	65 5e-10
<input type="checkbox"/>	sp Q32MK0	MYLK3_HUMAN Putative myosin light chain kinase 3 (EC 2...	64 7e-10
<input type="checkbox"/>	sp Q13233	M3K1_HUMAN Mitogen-activated protein kinase kinase kin...	64 7e-10
<input type="checkbox"/>	sp Q13555	KCC2G_HUMAN Calcium/calmodulin-dependent protein kinas...	64 7e-10
<input type="checkbox"/>	sp P22612	KAPCG_HUMAN cAMP-dependent protein kinase, gamma-catal...	64 7e-10
<input type="checkbox"/>	sp P36894	BMR1A_HUMAN Bone morphogenetic protein receptor type I...	64 7e-10
<input type="checkbox"/>	sp P20594	ANPRB_HUMAN Atrial natriuretic peptide receptor B prec...	64 7e-10

## Graphical overview of the alignments

[Click here](#) to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs  
 (Help) (use ScanProsite for more details about PROSITE matches)







Alignments

tr Q5BJG2 Fibroblast growth factor receptor 1 (Fms-related tyrosine kinase 2, 731 AA  
Q5BJG2\_HUMAN Pfeiffer syndrome) [FGFR1] [Homo sapiens (Human)] align

Score = 1420 bits (3677), Expect = 0.0  
Identities = 696/735 (94%), Positives = 709/735 (96%), Gaps = 6/735 (0%)

Query: 1 MWGWKCLLFWAVLVLTATLCTARPAPTLPEQDALPSSSEDDDDDDSSSEKETDNTKPNFV 60  
Sbjct: 1 MWSWKCLLFWAVLVLTATLCTARPSPTLPEQDALPSSSEDDDDDDSSSEKETDNTKPNFV 60

Query: 61 APYWTSPEKMEKKLHAVPAAKTVKFKCPSSSGTPNPTRLWLKNGKEFKPDHRIGGYKVRYA 120  
Sbjct: 61 APYWTSPEKMEKKLHAVPAAKTVKFKCPSSSGTPNPTRLWLKNGKEFKPDHRIGGYKVRYA 120

Query: 121 TWSIIMDSVVPFSDKGNITCIVENEYGSINHTYQLDVVERSHPRPILQAGLPANKTVALGS 180  
Sbjct: 121 TWSIIMDSVVPFSDKGNITCIVENEYGSINHTYQLDVVERSHPRPILQAGLPANKTVALGS 180

Query: 181 NVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKHSINSSDAE--VLTLPNV 238  
Sbjct: 181 NVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILK+G+NT+D E VL L NV 240

Query: 239 TEAQSGEYVCKVSNYIGEANQSAWLTVTRPVAKALEERPAMVTSPLYLEII IYCTGAFLI 298  
Sbjct: 241 SFEDAGEYTCLAGNSIGLSHSAWLTVL---EALERPAMVTSPLYLEII IYCTGAFLI 296

Query: 299 SCMLGSVVIYKMKSGTKKSDPHSQMAVHKLAISIPLRRQVTVSADSSASMSGVLLVRPS 358  
Sbjct: 297 SCMVGSVVIYKMKSGTKKSDPHSQMAVHKLAISIPLRRQVTVSADSSASMSGVLLVRPS 356

Query: 359 RLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGBGCFQGVVLAEEAIGLDKDKPFR 418  
Sbjct: 357 RLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGBGCFQGVVLAEEAIGLDKDKPFR 416

Query: 419 VTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHNIINLLEACTQDGPLYVIVEYASKG 478  
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Query: 479 NLREYLQARRPPGLEIYCYNPSHNPEEQQLSSKDLVSCAYQVARGMEYLASKKCIHRDLAAR 538  
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Sbjct: 537 NVLVTEDNVMKIADFGLARDIHHIDYKKTNGRLPVKWMAPALFDRIYTHQSDVWSFG 596

Query: 599 VLLWEIPTLGGSPYPGVPVEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTF 658  
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Query: 659 KQLVEVLDRIVALTSNQEYLDLS+PLDQYSPSPFDPTRSSSTCSSGEDSVFSHEPLPEEPCL 718  
Sbjct: 657 KQLVEDLDRIVALTSNQEYLDLSMPLDQYSPSPFDPTRSSSTCSSGEDSVFSHEPLPEEPCL 716

Query: 719 PRHPTQLANGSLKRR 733  
 PRHP QLAN GLKRR  
 Sbjct: 717 PRHPAQLANGSLKRR 731

sp\_vs P11362-14 Isoform 15 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 731 AA  
 FGFR1\_HUMAN (Human)] align

Score = 1420 bits (3677), Expect = 0.0  
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Query: 1 MWGKCLLFWAVLVLTATLCTARPAATLPEQDALPSSSEDDDDDDSSSEKETDNTKPNPV 60  
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 Sbjct: 1 MWSWKCLLFWAVLVLTATLCTARPSPTLPEQDALPSSSEDDDDDDSSSEKETDNTKPNPV 60

Query: 61 APYWTSPKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA 120  
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Query: 121 TWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQLDVVERSPhRPILQAGLPANKTVALGS 180  
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 Sbjct: 121 TWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQLDVVERSPhRPILQAGLPANKTVALGS 180

Query: 181 NVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPHYVQILKHSINSSDAE--VLTLFNV 238  
 NVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPHYVQILK +G+N++D E VL L NV  
 Sbjct: 181 NVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPHYVQILKTAGVNTTDKEMEVLHLRNV 240

Query: 239 TEAQSGEYVCKVSNYIGEANQSAWLTVTRPVAKALEERPAVMTSPYLEIIIIYCTGAFLI 298  
 + +GEY C N IG ++ SAWLTV +ALEERPAVMTSPYLEIIIIYCTGAFLI  
 Sbjct: 241 SFDADAGEYTCLAGNSIGLSHSAWLTVL----EALERPAVMTSPYLEIIIIYCTGAFLI 296

Query: 299 SCMLGSGVIYKMKSGTKKSDFHSSQMAVHKLAKSIPLRRQVTVSADSSASMSNGVLLVRPS 358  
 SCM+GSVI+YKMKSGTKKSDFHSSQMAVHKLAKSIPLRRQVTVSADSSASMSNGVLLVRPS  
 Sbjct: 297 SCMLGSGVIYKMKSGTKKSDFHSSQMAVHKLAKSIPLRRQVTVSADSSASMSNGVLLVRPS 356

Query: 359 RLSSSGTFLMAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAAEIGLDKDKPNR 418  
 RLSSSGTFLMAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAAEIGLDKDKPNR  
 Sbjct: 357 RLSSSGTFLMAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAAEIGLDKDKPNR 416

Query: 419 VTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIINLLEACTQDGPLYVIVEYASKG 478  
 VTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIINLL ACTQDGPLYVIVEYASKG  
 Sbjct: 417 VTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIINLLGACTQDGPLYVIVEYASKG 476

Query: 479 NLREYLQARRPPGLECYNPSHNPEEQLSKDLVSCAYQVARGMEYLASKKCIHRDLAAR 538  
 NLREYLQARRPPGLECYNPSHNPEEQLSKDLVSCAYQVARGMEYLASKKCIHRDLAAR  
 Sbjct: 477 NLREYLQARRPPGLECYNPSHNPEEQLSKDLVSCAYQVARGMEYLASKKCIHRDLAAR 536

Query: 539 NVLVTEDNVMKIADFGFLARDIHHIDYKKTNGRLPVKWMAPALFDRIYTHQSDVWSFG 598  
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 Sbjct: 537 NVLVTEDNVMKIADFGFLARDIHHIDYKKTNGRLPVKWMAPALFDRIYTHQSDVWSFG 596

Query: 599 VLLWEIPTLGGSPYPGPVVEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTF 658  
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Query: 659 KQLVEVLDRIVALTSNQEYLDLSIPLDQYSPSPFPDTRSSSTCSSGEDSVFSHEPLPEEPCL 718  
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 Sbjct: 657 KQLVEDLDRIVALTSNQEYLDLSMPLDQYSPSPFPDTRSSSTCSSGEDSVFSHEPLPEEPCL 716

Query: 719 PRHPTQLANGSLKRR 733  
 PRHP QLAN GLKRR  
 Sbjct: 717 PRHPAQLANGSLKRR 731

sp\_vs P11362-3 Isoform 6 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 733 AA  
 FGFR1\_HUMAN (Human)] align

Score = 1415 bits (3664), Expect = 0.0  
 Identities = 696/737 (94%), Positives = 709/737 (96%), Gaps = 8/737 (1%)

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 MW WKCLLFWAVLVLTATLCTARPA+PTLPEQDALPSSSEDDDDDDSSSEKETDNTKPN  
 Sbjct: 1 MWSWKCLLFWAVLVLTATLCTARPSPTLPEQDALPSSSEDDDDDDSSSEKETDNTKPNRM 60

Query: 59 PVAPYWTSPKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVR 118  
 PVAPYWTSPKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVR  
 Sbjct: 61 PVAPYWTSPKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVR 120

Query: 119 YATWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQLDVVERSPhRPILQAGLPANKTVAL 178  
 YATWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQLDVVERSPhRPILQAGLPANKTVAL  
 Sbjct: 121 YATWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQLDVVERSPhRPILQAGLPANKTVAL 180

```

Query: 179 GSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPHYVQILKHSGINSSDAE--VLTLF 236
          GSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPHYVQILK +G+N++D E VL L
Sbjct: 181 GSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPHYVQILKTAGVNTTDKEMEVLHLR 240

Query: 237 NVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVAKALEERPAVMTSPLYLEIIIIYCTGAF 296
          NV+ +GEY C N IG ++ SAWLTV +ALEERPAVMTSPLYLEIIIIYCTGAF
Sbjct: 241 NVSFEDAGEYTCLAGNSIGLSHSAWLTVL---EALEERPAVMTSPLYLEIIIIYCTGAF 296

Query: 297 LISCMGSGVIIYKMKSGTKKSDPHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVR 356
          LISCM+GSVI+YKMKSGTKKSDPHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVR
Sbjct: 297 LISCMVGSVIVYKMKSGTKKSDPHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVR 356

Query: 357 PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEIAGLDKDKP 416
          PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEIAGLDKDKP
Sbjct: 357 PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEIAGLDKDKP 416

Query: 417 NRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIIINLLEACTQDGPLYVIVEYAS 476
          NRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIIINL ACTQDGPLYVIVEYAS
Sbjct: 417 NRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIIINL GACTQDGPLYVIVEYAS 476

Query: 477 KGNLREYLQARRPPGLECYNPSHNPEEQLSKDLVSCAYQVARGMEYLASKKCIHRDLA 536
          KGNLREYLQARRPPGLECYNPSHNPEEQLSKDLVSCAYQVARGMEYLASKKCIHRDLA
Sbjct: 477 KGNLREYLQARRPPGLECYNPSHNPEEQLSKDLVSCAYQVARGMEYLASKKCIHRDLA 536

Query: 537 ARNVLVTEDNVMKIADFGGLARDIHHIDYKKTNGRLPVKWMPEALFDRIYTHQSDVWS 596
          ARNVLVTEDNVMKIADFGGLARDIHHIDYKKTNGRLPVKWMPEALFDRIYTHQSDVWS
Sbjct: 537 ARNVLVTEDNVMKIADFGGLARDIHHIDYKKTNGRLPVKWMPEALFDRIYTHQSDVWS 596

Query: 597 FGVLLWEIFTLGGSPYGPVPEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRP 656
          FGVLLWEIFTLGGSPYGPVPEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRP
Sbjct: 597 FGVLLWEIFTLGGSPYGPVPEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRP 656

Query: 657 TFKQLVEVLDRIVALTSNQEYLDLSIPLDQYSPSPDTRSSSTCSSGEDSVFSHEPLPEEP 716
          TFKQLVE LDRIVALTSNQEYLDLS+PLDQYSPSPDTRSSSTCSSGEDSVFSHEPLPEEP
Sbjct: 657 TFKQLVEDLDRIVALTSNQEYLDLSMPLDQYSPSPDTRSSSTCSSGEDSVFSHEPLPEEP 716

Query: 717 CLPRHPTQLANSGLKRR 733
          CLPRHP QLAN GLKRR
Sbjct: 717 CLPRHPAQLANGGLKRR 733

```

sp\_vs P11362-4 Isoform 8 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 731 AA  
 FGFR1\_HUMAN (Human)] align

Score = 1407 bits (3642), Expect = 0.0  
 Identities = 694/737 (94%), Positives = 707/737 (95%), Gaps = 10/737 (1%)

```

Query: 1 MWGWKCLLFWAVLVTATLCTARPAPTLPEQDALPSSSEDDDDDDSSSEKETDNTKPN-- 58
          MW WKCLLFWAVLVTATLCTARP+PTLPEQDALPSSSEDDDDDDSSSEKETDNTKPN
Sbjct: 1 MWGWKCLLFWAVLVTATLCTARPSPPTLPEQDALPSSSEDDDDDDSSSEKETDNTKPNRM 60

Query: 59 PVAPYWTSPKEKMKLLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVR 118
          PVAPYWTSPKEKMKLLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVR
Sbjct: 61 PVAPYWTSPKEKMKLLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVR 120

Query: 119 YATWSIIMDSVVPVSDKGNYSICIVENEYGSINHTYQLDVVERSHPHRPILQAGLPANKTVAL 178
          YATWSIIMDSVVPVSDKGNYSICIVENEYGSINHTYQLDVVERSHPHRPILQAGLPANKTVAL
Sbjct: 121 YATWSIIMDSVVPVSDKGNYSICIVENEYGSINHTYQLDVVERSHPHRPILQAGLPANKTVAL 180

Query: 179 GSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPHYVQILKHSGINSSDAE--VLTLF 236
          GSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPHYVQILK +G+N++D E VL L
Sbjct: 181 GSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPHYVQILKTAGVNTTDKEMEVLHLR 240

Query: 237 NVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVAKALEERPAVMTSPLYLEIIIIYCTGAF 296
          NV+ +GEY C N IG ++ SAWLTV +ALEERPAVMTSPLYLEIIIIYCTGAF
Sbjct: 241 NVSFEDAGEYTCLAGNSIGLSHSAWLTVL---EALEERPAVMTSPLYLEIIIIYCTGAF 296

Query: 297 LISCMGSGVIIYKMKSGTKKSDPHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVR 356
          LISCM+GSVI+YKMKSGTKKSDPHSQMAVHKLAKSIPLRRQV SADSSASMNSGVLLVR
Sbjct: 297 LISCMVGSVIVYKMKSGTKKSDPHSQMAVHKLAKSIPLRRQV--SADSSASMNSGVLLVR 354

Query: 357 PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEIAGLDKDKP 416
          PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEIAGLDKDKP
Sbjct: 355 PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEIAGLDKDKP 414

Query: 417 NRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIIINLLEACTQDGPLYVIVEYAS 476
          NRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIIINL ACTQDGPLYVIVEYAS
Sbjct: 415 NRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIIINL GACTQDGPLYVIVEYAS 474

Query: 477 KGNLREYLQARRPPGLECYNPSHNPEEQLSKDLVSCAYQVARGMEYLASKKCIHRDLA 536
          KGNLREYLQARRPPGLECYNPSHNPEEQLSKDLVSCAYQVARGMEYLASKKCIHRDLA
Sbjct: 475 KGNLREYLQARRPPGLECYNPSHNPEEQLSKDLVSCAYQVARGMEYLASKKCIHRDLA 534

Query: 537 ARNVLVTEDNVMKIADFGGLARDIHHIDYKKTNGRLPVKWMPEALFDRIYTHQSDVWS 596

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          ARNVLVTEEDNMVKIADFGGLARDIHHIDYKKTTNGRLPVKWMPEALFDRIYTHQSDVWS
Sbjct: 535 ARNVLVTEEDNMVKIADFGGLARDIHHIDYKKTTNGRLPVKWMPEALFDRIYTHQSDVWS 594

Query: 597 FGVLLWEIFTLGGSPYPGVVPEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRP 656
          FGVLLWEIFTLGGSPYPGVVPEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRP
Sbjct: 595 FGVLLWEIFTLGGSPYPGVVPEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRP 654

Query: 657 TFKQLVEVLDRIVALTSNQEYLDLSIFLDQYSPSPDTRSSSTCSSGEDSVFSHEPLPEEP 716
          TFKQLVE LDRIVALTSNQEYLDLS+PLDQYSPSPDTRSSSTCSSGEDSVFSHEPLPEEP
Sbjct: 655 TFKQLVEDLDRIVALTSNQEYLDLSMPLDQYSPSPDTRSSSTCSSGEDSVFSHEPLPEEP 714

Query: 717 CLPRHPTQLANSGLKRR 733
          CLPRHP QLAN GLKRR
Sbjct: 715 CLPRHPAQLANGGLKRR 731

```

```

sp_vs P11362-7      Isoform 14 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 820 AA
FGFR1_HUMAN      (Human)] align

```

Score = 1357 bits (3513), Expect = 0.0  
Identities = 668/705 (94%), Positives = 680/705 (96%), Gaps = 6/705 (0%)

```

Query: 31  DALPSSDDDDDDSSSEKETDNTKPNVPAPYWTSPKMEKKLHAVPAAKTVKFKCPSS 90
          DALPSSDDDDDDSSSEKETDNTKPNVPAPYWTSPKMEKKLHAVPAAKTVKFKCPSS
Sbjct: 120 DALPSSDDDDDDSSSEKETDNTKPNVPAPYWTSPKMEKKLHAVPAAKTVKFKCPSS 179

Query: 91  GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSINH 150
          GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSINH
Sbjct: 180 GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSINH 239

Query: 151 TYQLDVVERSHPHPILOAGLPANKTVALGNSVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
          TYQLDVVERSHPHPILOAGLPANKTVALGNSVEFMCKVYSDPQPHIQWLKHIEVNGSKIG
Sbjct: 240 TYQLDVVERSHPHPILOAGLPANKTVALGNSVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 299

Query: 211 PDNLPPYQILKHSGINSDDAE--VLTLFNVTEAQSGEYVCKVSNYIGEANSAWLTVTRP 268
          PDNLPPYQILK +G+N++D E VL L NV+ +GEY C N IG ++ SAWLTV
Sbjct: 300 PDNLPPYQILKTAGVNTTDKEMEVLHLRNVSPEDAGEYTCLAGNSIGLSHHSAWLTVL-- 357

Query: 269 VAKALEERPAMVTSPLYLEIIIIYCTGAFLISCMGSVIYKMKSGTKKSDFHSQMAVHKL 328
          +ALEERPAMVTSPLYLEIIIIYCTGAFLISCM+GSVI+YKMKSGTKKSDFHSQMAVHKL
Sbjct: 358 --EALERPAMVTSPLYLEIIIIYCTGAFLISCMVGSVIVYKMKSGTKKSDFHSQMAVHKL 415

Query: 329 AKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDR 388
          AKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDR
Sbjct: 416 AKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDR 475

Query: 389 LVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKM 448
          LVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKM
Sbjct: 476 LVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKM 535

Query: 449 IGKHKNIIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQQLSS 508
          IGKHKNIIINLL ACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQQLSS
Sbjct: 536 IGKHKNIIINLLGACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQQLSS 595

Query: 509 KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEEDNMVKIADFGGLARDIHHIDYKKTT 568
          KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEEDNMVKIADFGGLARDIHHIDYKKTT
Sbjct: 596 KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEEDNMVKIADFGGLARDIHHIDYKKTT 655

Query: 569 TNGRLPVKWMPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVVPEELFKLLKEGH 628
          TNGRLPVKWMPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVVPEELFKLLKEGH
Sbjct: 656 TNGRLPVKWMPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVVPEELFKLLKEGH 715

Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPFTFKQLVEVLDRIVALTSNQEYLDLSIFLDQYS 688
          RMDKPSNCTNELYMMMRDCWHAVPSQRPFTFKQLVE LDRIVALTSNQEYLDLS+PLDQYS
Sbjct: 716 RMDKPSNCTNELYMMMRDCWHAVPSQRPFTFKQLVEDLDRIVALTSNQEYLDLSMPLDQYS 775

Query: 689 PSFPDTRSSSTCSSGEDSVFSHEPLPEEPCLPRHPTQLANSGLKRR 733
          PSFPDTRSSSTCSSGEDSVFSHEPLPEEPCLPRHP QLAN GLKRR
Sbjct: 776 PSFPDTRSSSTCSSGEDSVFSHEPLPEEPCLPRHPAQLANGGLKRR 820

```

Score = 91.3 bits (225), Expect = 5e-18  
Identities = 78/305 (25%), Positives = 118/305 (38%), Gaps = 81/305 (26%)

```

Query: 1  MWGWKCLLFWAVLVLTATLCTARPAPTLPEQDALPSSDDDDDDSSSEKETDNTKPNVP 60
          MW WKCLLFWAVLVLTATLCTARP+PTLPEQ
Sbjct: 1  MWSWKCLLFWAVLVLTATLCTARPSPTLPEQ----- 30

Query: 61  APYWTSPKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA 120
          A W +P ++E L V ++ +C ++ WL++G + +R R
Sbjct: 31  AQPNGAPVEVESFL--VHPGDLQLRCRLRDDVQ-SINWLRDGVQLAESNR-----TRIT 82

Query: 121 TWSIIMDSVVP SDKGNYTCIVENEYGSINH TYQLDVVERSHPH----- 162
          + + VP+D G Y C+ + GS + ++V + P
Sbjct: 83  GEEVEVQDSVPADSGLYACVTSSPSGSDTTYFSVNVSDALPSSDDDDDDSSSEKETD 142

```

```

Query: 163 ----RPILQAGLPANK-----TVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPD 212
      P+      K      V      V+F C      P P ++WLK      NG + PD
Sbjct: 143 NTKPNPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLK----NGKEFKPD 198

Query: 213 NLPYVQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVT-----R 267
      +      ++++ +      + + +V + G Y C V N G N + L V      R
Sbjct: 199 HRIGGYKVRYATWS-----IIMDSVVP SDKGNYTCIVENEYGSINHTYQLDVVERSPHR 252

Query: 268 PVAKA 272
      P+ +A
Sbjct: 253 PILQA 257

```

```

sp P11362      Basic fibroblast growth factor receptor 1 precursor (EC 2.7.10.1) 822 AA
FGFR1_HUMAN (FGFR-1) (bFGF-R) (Fms-like tyrosine kinase 2) (c-fgr) align
      (CD331 antigen) [FGFR1] [Homo sapiens (Human)]

```

Score = 1352 bits (3500), Expect = 0.0  
 Identities = 668/707 (94%), Positives = 680/707 (96%), Gaps = 8/707 (1%)

```

Query: 31 DALPSSDDDDDDSSSEKETDNTKPN--PVAPYWTSPEKMEKKLHAVPAAKTVKFKCP 88
      DALPSSDDDDDDSSSEKETDNTKPN PVAPYWTSPEKMEKKLHAVPAAKTVKFKCP
Sbjct: 120 DALPSSDDDDDDSSSEKETDNTKPNRMPVAPYWTSPEKMEKKLHAVPAAKTVKFKCP 179

Query: 89 SSGTFNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSI 148
      SSGTFNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSI
Sbjct: 180 SSGTFNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSI 239

Query: 149 NHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSK 208
      NHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSK
Sbjct: 240 NHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSK 299

Query: 209 IGPDNLPYVQILKHSGINSSDAE--VLTILFNVTEAQSGEYVCKVSNYIGEANQSAWLTVT 266
      IGPDNLPYVQILK +G+N++D E VL L NV+ +GEY C N IG ++ SAWLTV
Sbjct: 300 IGPDNLPYVQILKTAGVNTTDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVL 359

Query: 267 RPVAKALEERPAMVMTSPLYLEIIIIYCTGAFLISCMVGSVVIYKMKSGTKKSDPHSQMAVH 326
      +ALEERPAMVMTSPLYLEIIIIYCTGAFLISCM+GSVI+YKMKSGTKKSDPHSQMAVH
Sbjct: 360 ----EALERPAMVMTSPLYLEIIIIYCTGAFLISCMVGSVVIYKMKSGTKKSDPHSQMAVH 415

Query: 327 KLAKSIPLRQVTVSADSSASMSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR 386
      KLAKSIPLRQVTVSADSSASMSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR
Sbjct: 416 KLAKSIPLRQVTVSADSSASMSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR 475

Query: 387 DRLVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 446
      DRLVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM
Sbjct: 476 DRLVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 535

Query: 447 KMIGKHKNIINLLACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEQL 506
      KMIGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEQL
Sbjct: 536 KMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEQL 595

Query: 507 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADPGLARDIHHIDYK 566
      SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADPGLARDIHHIDYK
Sbjct: 596 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADPGLARDIHHIDYK 655

Query: 567 KTTNGRPLVKKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPVEELFKLLKE 626
      KTTNGRPLVKKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPVEELFKLLKE
Sbjct: 656 KTTNGRPLVKKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPVEELFKLLKE 715

Query: 627 GHRMDKPSNCTNELYMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQ 686
      GHRMDKPSNCTNELYMMRDCWHAVPSQRPTFKQLVE LDRIVALTSNQEYLDLS+PLDQ
Sbjct: 716 GHRMDKPSNCTNELYMMRDCWHAVPSQRPTFKQLVEDLDRIVALTSNQEYLDLSMPLDQ 775

Query: 687 YSPSFPDTRSSSTCSSGEDSVFSHEPLPEEPCLPRHPTQLANSGLKRR 733
      YSPSFPDTRSSSTCSSGEDSVFSHEPLPEEPCLPRHP QLANS GLKRR
Sbjct: 776 YSPSFPDTRSSSTCSSGEDSVFSHEPLPEEPCLPRHPAQLANGGLKRR 822

```

Score = 90.5 bits (223), Expect = 9e-18  
 Identities = 78/307 (25%), Positives = 118/307 (38%), Gaps = 83/307 (27%)

```

Query: 1 MWGWKCLLFWAVLVLTATLCTARPAPTLPEQDALPSSDDDDDDSSSEKETDNTKPNPV 60
      MW WKCLLFWAVLVLTATLCTARP+PTLPEQ
Sbjct: 1 MWSWKCLLFWAVLVLTATLCTARPSPTLPEQ----- 30

Query: 61 APYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA 120
      A W +P ++E L V ++ +C ++ WL++G + +R R
Sbjct: 31 AQPWGAPVEVESFL--VHPGDLQLRLRDDVQ--SINWLRDGVQLAESNR-----TRIT 82

Query: 121 TWSIIMDSVVP SDKGNYTCIVENEYGSINHTYQLDVVERSP----- 161
      + + VP+D G Y C+ + GS + ++V + P
Sbjct: 83 GEEVEVQDVPADSGLYACVTSSPSGSDTTYFSVNVSDALPSSDDDDDDSSSEKETD 142

```

```

Query: 162 -----HRPILQAGLPANK-----TVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
          P+          K          V          V+F C          P P ++WLK          NG +
Sbjct: 143 NTKPNRMPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLK---NGKEFK 198

Query: 211 PDNLPHYQILKHSGINSDDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVT---- 266
          PD+          ++++ +          + + +V + G Y C V N G N + L V
Sbjct: 199 PDHRIGGYKVRYATWS-----IIMDSVVP SDKGNYTCIVENEYGSINHTYQLDVVERSP 252

Query: 267 -RPVAKA 272
          RP+ +A
Sbjct: 253 HRPILQA 259

```

```

tr Q53H63      Fibroblast growth factor receptor 1 isoform 2 variant (Fragment) 820 AA
Q53H63_HUMAN  [Homo sapiens (Human)] align

```

Score = 1351 bits (3496), Expect = 0.0  
 Identities = 665/705 (94%), Positives = 678/705 (96%), Gaps = 6/705 (0%)

```

Query: 31  DALPSSDDDDDDSSSEKETDNTKPNFVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSS 90
          DALPSSDDDDDDSSSEKETDNTKPNFVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSS
Sbjct: 120 DALPSSDDDDDDSSSEKETDNTKPNFVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSS 179

Query: 91  GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSINH 150
          GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP  DKGNYTCIVENEYGSINH
Sbjct: 180 GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP DKGNYTCIVENEYGSINH 239

Query: 151 TYQLDVVERSPHRPILQAGLPANKTVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
          TYQLDVVERSPHRPILQAGLPANKTVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG
Sbjct: 240 TYQLDVVERSPHRPILQAGLPANKTVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 299

Query: 211 PDNLPHYQILKHSGINSDDAE--VLTFLNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRP 268
          PDNLPHYQILK +G+N++D E VL L NV+ +GEY C N IG ++ SAWLTV
Sbjct: 300 PDNLPHYQILKTAGVNTTDKEMEVLHLRNVSPEDAGEYTCLAGNSIGLSHHSWLTVL-- 357

Query: 269 VAKALEERPAMVMTSPLYLEIIYCTGAPLISCMGSVIIYKMKSGTKKSDFHQSQMAVHKL 328
          +ALEERPAMVMTSPLYLEIIYCTGAPLISCM+GSVI+YKMKSGTKKSDFHQSQMAVHKL
Sbjct: 358 --BALEERPAMVMTSPLYLEIIYCTGAPLISCMVGSVIVYKMKSGTKKSDFHQSQMAVHKL 415

Query: 329 AKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDR 388
          AKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDR
Sbjct: 416 AKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDR 475

Query: 389 LVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKM 448
          LVLG+PLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKM
Sbjct: 476 LVLGRPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKM 535

Query: 449 IGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQQLSS 508
          IGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYLQA RPPGLECYNPSHNPEEQQLSS
Sbjct: 536 IGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLQAWRPPGLECYNPSHNPEEQQLSS 595

Query: 509 KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNMKIADFGGLARDIHHIDYYKKT 568
          KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNMKIADFGGLARDIHHIDYYKKT
Sbjct: 596 KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNMKIADFGGLARDIHHIDYYKKT 655

Query: 569 TNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGH 628
          TNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGH
Sbjct: 656 TNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGH 715

Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQYS 688
          RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRIVALTSNQEYLDLS+PLDQYS
Sbjct: 716 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRIVALTSNQEYLDLSMPLDQYS 775

Query: 689 PSFPDTRSSSTCSSGEDSVFSHEPLPEEPCLPRHPTQLANSGLKRR 733
          PSFPDTRSSSTCSSGEDSVFSHEPLPEEPCLPRHP QLAN GLKRR
Sbjct: 776 PSFPDTRSSSTCSSGEDSVFSHEPLPEEPCLPRHPAQLANGGLKRR 820

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Score = 90.1 bits (222), Expect = 1e-17  
 Identities = 78/305 (25%), Positives = 117/305 (38%), Gaps = 81/305 (26%)

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Query: 1  MWGWKCLLFWAVLVTATLCTARPAPTLPEQDALPSSDDDDDDSSSEKETDNTKPNPV 60
          MW WKCLLFWAVLVTATLCTARP+PTLPEQ
Sbjct: 1  MWSWKCLLFWAVLVTATLCTARPSPTLPEQ----- 30

Query: 61  APYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA 120
          A W +P ++E L V ++ +C ++ WL++G + ++R R
Sbjct: 31  AQPWGAPEVESFL--VHPGDLLQLRCRLRDDVQ-SINWLRDGVQLAESNR-----TRIT 82

Query: 121 TWSIIMDSVVP SDKGNYTCIVENEYGSINHTYQLDVVERSP----- 162
          + + VP+D G Y C+ + GS + ++V + P
Sbjct: 83  GEEVEVQDSVPADSGLYACVTSSPSGSDTTYFSVNVSDALPSSDDDDDDSSSEKETD 142

Query: 163 ----RPILQAGLPANK-----TVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPD 212
          P+          K          V          V+F C          P P ++WLK          NG + PD

```

```
Sbjct: 143 NTKPNPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLK---NGKEFKPD 198

Query: 213 NLPYVQILKHSINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVT----R 267
      +      +++++ +      + + +V      G Y C V N G N + L V      R
Sbjct: 199 HRIGGYKVRVYATWS-----IIMDSVVPFDKGNVTCIVENEYGSINHTYQLDVVERSPhR 252

Query: 268 PVAKA 272
      P+ +A
Sbjct: 253 PILQA 257

tr Q59H40      Fibroblast growth factor receptor 1 isoform 1 variant (Fragment) 814 AA
Q59H40_HUMAN  [Homo sapiens (Human)]      align

Score = 1344 bits (3478), Expect = 0.0
Identities = 666/707 (94%), Positives = 678/707 (95%), Gaps = 10/707 (1%)

Query: 31 DALPSSDDDDDDSSSEKETDNTKPN--PVAPYWTSPEKMEKKLHAVPAAKTVKFKCP 88
      DALPSSDDDDDDSSSEKETDNTKPN PVAPYWTSPEKMEKKLHAVPAAKTVKFKCP
Sbjct: 114 DALPSSDDDDDDSSSEKETDNTKPNRMPVAPYWTSPEKMEKKLHAVPAAKTVKFKCP 173

Query: 89 SSGTPNPTLRWLKNGKEFKPDHRIGGYKVRVYATWSIIMDSVVPDCKGNVTCIVENEYGSI 148
      SSGTPNPTLRWLKNGKEFKPDHRIGGYKVRVYATWSIIMDSVVPDCKGNVTCIVENEYGSI
Sbjct: 174 SSGTPNPTLRWLKNGKEFKPDHRIGGYKVRVYATWSIIMDSVVPDCKGNVTCIVENEYGSI 233

Query: 149 NHTYQLDVVERSPhRPILQAGLPANKTVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSK 208
      NHTYQLDVVERSPhRPILQAGLPANKTVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSK
Sbjct: 234 NHTYQLDVVERSPhRPILQAGLPANKTVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSK 293

Query: 209 IGPDLNLPYVQILKHSINSSDAE--VLTFLNVTEAQSGEYVCKVSNYIGEANQSAWLTVT 266
      IGPDLNLPYVQILK +G+N++D E VL L NV+ +GEY C N IG ++ SAWLTV
Sbjct: 294 IGPDLNLPYVQILKTAGVNTTDKEMEVLHLRNVSPEDAGEYTCLAGNSIGLSHHSAWLTVL 353

Query: 267 RPVAKALEERPFAVMTSPLYLEIIIIYCTGAFLISCMGSVIIYKMKSGTKKSDFHSQMAVH 326
      +ALEERPFAVMTSPLYLEIIIIYCTGAFLISCM+GSVI+YKMKSGTKKSDFHSQMAVH
Sbjct: 354 ----EALERPFAVMTSPLYLEIIIIYCTGAFLISCMVGSVIVYKMKSGTKKSDFHSQMAVH 409

Query: 327 KLAKSIPLRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR 386
      KLAKSIPLRQV SADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR
Sbjct: 410 KLAKSIPLRQV--SADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR 467

Query: 387 DRLVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 446
      DRLVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM
Sbjct: 468 DRLVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 527

Query: 447 KMIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLEICYNPSHNPEEQ 506
      KMIGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYLQARRPPGLEICYNPSHNPEEQ
Sbjct: 528 KMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLQARRPPGLEICYNPSHNPEEQ 587

Query: 507 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADPGLARDIHHIDYK 566
      SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADPGLARDIHHIDYK
Sbjct: 588 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADPGLARDIHHIDYK 647

Query: 567 KTTNGRLPVKWMPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPEELFKLLKE 626
      KTTNGRLPVKWMPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPEELFKLLKE
Sbjct: 648 KTTNGRLPVKWMPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPEELFKLLKE 707

Query: 627 GHRMDKPSNCTNELYMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQ 686
      GHRMDKPSNCTNELYMMRDCWHAVPSQRPTFKQLVE LDRIVALTSNQEYLDLS+PLDQ
Sbjct: 708 GHRMDKPSNCTNELYMMRDCWHAVPSQRPTFKQLVEDLDRIVALTSNQEYLDLSMPLDQ 767

Query: 687 YSPSFPDTRSSSTCSSGSDSVFSHEPLPEEPCLPRHPTQLANGSLKRR 733
      YSPSFPDTRSSSTCSSGSDSVFSHEPLPEEPCLPRHP QLAN GLKRR
Sbjct: 768 YSPSFPDTRSSSTCSSGSDSVFSHEPLPEEPCLPRHPAQLANGSLKRR 814

Score = 43.1 bits (100), Expect = 0.002
Identities = 49/244 (20%), Positives = 88/244 (36%), Gaps = 53/244 (21%)

Query: 64 WTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRVYATWS 123
      W +P ++E L V ++ +C ++ WL++G + +R R
Sbjct: 28 WGAPVEVESFL--VHPGDLQLRCRLRDDVQ-SINWLRDGVQLAESNR-----TRITGEE 79

Query: 124 IIMDSVVPDCKGNVTCIVENEYGSINHTYQLDVVERS----- 161
      + + VF+D G Y C+ + GS + ++V + P
Sbjct: 80 VEQDSVPADSGLYACVTSSPSGSDTTYFSVNVSDALPSSDDDDDDSSSEKETDNTK 139

Query: 162 --HRPILQAGLPANK-----TVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDN 213
      P+ K V V+P C P P ++WLK NG + PD+
Sbjct: 140 PNRMPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLK---NGKEFKPDH 195

Query: 214 LPYVQILKHSINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVT----RP 268
      +++++ + + + +V + G Y C V N G N + L V RP
Sbjct: 196 RIGGYKVRVYATWS-----IIMDSVVPDCKGNVTCIVENEYGSINHTYQLDVVERSPhR 249
```

Query: 269 VAKA 272  
+ +A  
Sbjct: 250 ILQA 253

sp\_vs P11362-2 Isoform 4 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 820 AA  
FGFR1\_HUMAN (Human)] align

Score = 1344 bits (3478), Expect = 0.0  
Identities = 666/707 (94%), Positives = 678/707 (95%), Gaps = 10/707 (1%)

Query: 31 DALPSSDDDDDDSSSEEEKETDNTKPN--PVAPYWTSPEKMEKKLHAVPAAKTVKFKCP 88  
DALPSSDDDDDDSSSEEEKETDNTKPN PVAPYWTSPEKMEKKLHAVPAAKTVKFKCP  
Sbjct: 120 DALPSSDDDDDDSSSEEEKETDNTKPNRMPVAPYWTSPEKMEKKLHAVPAAKTVKFKCP 179

Query: 89 SSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSI 148  
SSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSI  
Sbjct: 180 SSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSI 239

Query: 149 NHTYQLDVVERSHPRPILQAGLPANKTVALGNSVEFMCKVYSDPQPHIQWLKHIEVNGSK 208  
NHTYQLDVVERSHPRPILQAGLPANKTVALGNSVEFMCKVYSDPQPHIQWLKHIEVNGSK  
Sbjct: 240 NHTYQLDVVERSHPRPILQAGLPANKTVALGNSVEFMCKVYSDPQPHIQWLKHIEVNGSK 299

Query: 209 IGPDNLPYVQILKHSGINSSDAE--VLTFLFNVTQAQSGEYVCKVSNYIGEANQSAWLTVT 266  
IGPDNLPYVQILK +G+N++D E VL L NV+ +GEY C N IG ++ SAWLTV  
Sbjct: 300 IGPDNLPYVQILKTAGVNTTDKEMEVLHLRNVSPEDAGEYTCLAGNSIGLSHSAWLTVL 359

Query: 267 RPAKALEERPAVMTSPLYLEIIYCTGAFLISCMGSGVIYKMKSGTKKSDPHSQMAVH 326  
+ALEERPAVMTSPLYLEIIYCTGAFLISCM+GSGVI+YKMKSGTKKSDPHSQMAVH  
Sbjct: 360 ----EALERPAVMTSPLYLEIIYCTGAFLISCMVGSIVYKMKSGTKKSDPHSQMAVH 415

Query: 327 KLAKSIPLRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR 386  
KLAKSIPLRQV SADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR  
Sbjct: 416 KLAKSIPLRQV--SADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR 473

Query: 387 DRVLVGLKPLGEGCGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 446  
DRVLVGLKPLGEGCGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM  
Sbjct: 474 DRVLVGLKPLGEGCGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 533

Query: 447 KMIGKHKNIINLLACTQDGPLYVIVEYASKGNLREYQLQARRPPGLECYCYNPSHNPEEQ 506  
KMIGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYQLQARRPPGLECYCYNPSHNPEEQ  
Sbjct: 534 KMIGKHKNIINLLACTQDGPLYVIVEYASKGNLREYQLQARRPPGLECYCYNPSHNPEEQ 593

Query: 507 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLTEDNVMKIADPGLARDIHHIDYYK 566  
SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLTEDNVMKIADPGLARDIHHIDYYK  
Sbjct: 594 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLTEDNVMKIADPGLARDIHHIDYYK 653

Query: 567 KTTNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPEELFKLLKE 626  
KTTNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPEELFKLLKE  
Sbjct: 654 KTTNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPEELFKLLKE 713

Query: 627 GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQ 686  
GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRIVALTSNQEYLDLS+PLDQ  
Sbjct: 714 GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRIVALTSNQEYLDLSMPLDQ 773

Query: 687 YSPSPDTRSSSTCSSGEDSVFSHEPLPEEPCLPRHPTQLANSGLKRR 733  
YSPSPDTRSSSTCSSGEDSVFSHEPLPEEPCLPRHP QLAN GLKRR  
Sbjct: 774 YSPSPDTRSSSTCSSGEDSVFSHEPLPEEPCLPRHPAQLANGGLKRR 820

Score = 90.5 bits (223), Expect = 9e-18  
Identities = 78/307 (25%), Positives = 118/307 (38%), Gaps = 83/307 (27%)

Query: 1 MWGKCLLFWAVLVTATLCTARPAITLPEQDALPSSDDDDDDSSSEEEKETDNTKPNPV 60  
MW WKCLLFWAVLVTATLCTARP+PTLPEQ  
Sbjct: 1 MWSWKCLLFWAVLVTATLCTARPSPTLPEQ----- 30

Query: 61 APYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA 120  
A W +P ++E L V ++ +C ++ WL++G + +R R  
Sbjct: 31 AQPWGAPVEVESFL--VHPGDLLQLRCRLRDDVQ--SINWLRDGVQLAESNR-----TRIT 82

Query: 121 TWSIIMDSVVP SDKGNYTCIVENEYGSINHTYQLDVVERS----- 161  
+ + VP+D G Y C + + GS + ++V + P  
Sbjct: 83 GEEVEVQDSVPADSGLYACVTSSPSGSDTTYFSVNVSDALPSSDDDDDDSSSEEEKETD 142

Query: 162 -----HRFILQAGLPANK-----TVALGNSVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210  
P+ K V V+ F C P P ++WLK NG +  
Sbjct: 143 NTKPNRMPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLK----NGKEFK 198

Query: 211 PDNLPYVQILKHSGINSSDAEVLTLFNVTQAQSGEYVCKVSNYIGEANQSAWLTVT---- 266  
PD+ ++++ + + + +V + G Y C V N G N + L V  
Sbjct: 199 PDHRIGGYKVRYATWS-----IIMDSVVP SDKGNYTCIVENEYGSINHTYQLDVVERS 252

Query: 267 -RPVAKA 272  
RP+ +A



Sbjct: 253 HRPILQA 259

sp\_vs P11362-5 Isoform 10 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 662 AA  
 FGFR1\_HUMAN (Human)] align

Score = 1275 bits (3299), Expect = 0.0  
 Identities = 629/666 (94%), Positives = 641/666 (96%), Gaps = 6/666 (0%)

Query: 70 MEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRATWSIIMDSV 129  
 MEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRATWSIIMDSV  
 Sbjct: 1 MEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRATWSIIMDSV 60

Query: 130 VPSDKGNYTCIVENEYGSINHTYQLDVVERSHPRPILQAGLPANKTVALGNSNVEFMCKVY 189  
 VPSDKGNYTCIVENEYGSINHTYQLDVVERSHPRPILQAGLPANKTVALGNSNVEFMCKVY  
 Sbjct: 61 VPSDKGNYTCIVENEYGSINHTYQLDVVERSHPRPILQAGLPANKTVALGNSNVEFMCKVY 120

Query: 190 SDPQPHIQWLKHIEVNGSKIGPDNLFPYVQILKHSGINSSDAE--VLTFLFNVTQAQSGEYV 247  
 SDPQPHIQWLKHIEVNGSKIGPDNLFPYVQILK +G+N++D E VL L NV+ +GEY  
 Sbjct: 121 SDPQPHIQWLKHIEVNGSKIGPDNLFPYVQILKTAGVNTTDEKEMEVLHLRNVSFEDAGEYT 180

Query: 248 CKVSNYIGEANQSAWLTVTRPVAKALEERPAMVMTSPLYLEIIIIYCTGAFLISCMLGSVII 307  
 C N IG ++ SAWLTV +ALEERPAMVMTSPLYLEIIIIYCTGAFLISCM+GSVI+  
 Sbjct: 181 CLAGNSIGLSHHSWLTVL----EALERPAMVMTSPLYLEIIIIYCTGAFLISCMVGSVIV 236

Query: 308 YKMKSGTKKSDFHQSMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVVRPSRLSSSGTTPM 367  
 YKMKSGTKKSDFHQSMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVVRPSRLSSSGTTPM  
 Sbjct: 237 YKMKSGTKKSDFHQSMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVVRPSRLSSSGTTPM 296

Query: 368 LAGVSEYELPEDPRWELPRDLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKML 427  
 LAGVSEYELPEDPRWELPRDLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKML  
 Sbjct: 297 LAGVSEYELPEDPRWELPRDLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKML 356

Query: 428 KSDATEKDLSDLISEMEMMKMIGKHKNIIINLLEACTQDGPLYVIVEYASKGNLREYLQAR 487  
 KSDATEKDLSDLISEMEMMKMIGKHKNIIINLL ACTQDGPLYVIVEYASKGNLREYLQAR  
 Sbjct: 357 KSDATEKDLSDLISEMEMMKMIGKHKNIIINLLGACTQDGPLYVIVEYASKGNLREYLQAR 416

Query: 488 RPPGLECYNPNSHNPEEQQLSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNV 547  
 RPPGLECYNPNSHNPEEQQLSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNV  
 Sbjct: 417 RPPGLECYNPNSHNPEEQQLSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNV 476

Query: 548 MKIADFGGLARDIHHIDYYKKTNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIPTL 607  
 MKIADFGGLARDIHHIDYYKKTNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIPTL  
 Sbjct: 477 MKIADFGGLARDIHHIDYYKKTNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIPTL 536

Query: 608 GGSPPYPGVFVEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDLDR 667  
 GGSPPYPGVFVEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVE LDR  
 Sbjct: 537 GGSPPYPGVFVEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDR 596

Query: 668 IVALTSNQEYLDLS+PLDQYSPSPDTRSSSTCSSGEDSVFSHEPLPEEPCLPRHPTQLAN 727  
 IVALTSNQEYLDLS+PLDQYSPSPDTRSSSTCSSGEDSVFSHEPLPEEPCLPRHP QLAN  
 Sbjct: 597 IVALTSNQEYLDLS+PLDQYSPSPDTRSSSTCSSGEDSVFSHEPLPEEPCLPRHPAQLAN 656

Query: 728 SGLKRR 733  
 GLKRR  
 Sbjct: 657 GGLKRR 662

sp\_vs P11362-6 Isoform 12 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 660 AA  
 FGFR1\_HUMAN (Human)] align

Score = 1266 bits (3277), Expect = 0.0  
 Identities = 627/666 (94%), Positives = 639/666 (95%), Gaps = 8/666 (1%)

Query: 70 MEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRATWSIIMDSV 129  
 MEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRATWSIIMDSV  
 Sbjct: 1 MEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRATWSIIMDSV 60

Query: 130 VPSDKGNYTCIVENEYGSINHTYQLDVVERSHPRPILQAGLPANKTVALGNSNVEFMCKVY 189  
 VPSDKGNYTCIVENEYGSINHTYQLDVVERSHPRPILQAGLPANKTVALGNSNVEFMCKVY  
 Sbjct: 61 VPSDKGNYTCIVENEYGSINHTYQLDVVERSHPRPILQAGLPANKTVALGNSNVEFMCKVY 120

Query: 190 SDPQPHIQWLKHIEVNGSKIGPDNLFPYVQILKHSGINSSDAE--VLTFLFNVTQAQSGEYV 247  
 SDPQPHIQWLKHIEVNGSKIGPDNLFPYVQILK +G+N++D E VL L NV+ +GEY  
 Sbjct: 121 SDPQPHIQWLKHIEVNGSKIGPDNLFPYVQILKTAGVNTTDEKEMEVLHLRNVSFEDAGEYT 180

Query: 248 CKVSNYIGEANQSAWLTVTRPVAKALEERPAMVMTSPLYLEIIIIYCTGAFLISCMLGSVII 307  
 C N IG ++ SAWLTV +ALEERPAMVMTSPLYLEIIIIYCTGAFLISCM+GSVI+  
 Sbjct: 181 CLAGNSIGLSHHSWLTVL----EALERPAMVMTSPLYLEIIIIYCTGAFLISCMVGSVIV 236

Query: 308 YKMKSGTKKSDFHQSMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVVRPSRLSSSGTTPM 367

```

      YKMKSGTKKSDPHSQMAVHKLAKSIPLRRQV  SADSSASMNSGVLLVRPSRLSSSGTPM
Sbjct: 237 YKMKSGTKKSDPHSQMAVHKLAKSIPLRRQV--SADSSASMNSGVLLVRPSRLSSSGTPM 294

      LAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEIAGLDKDKPNRVTKVAVKML 427
      LAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEIAGLDKDKPNRVTKVAVKML
Sbjct: 295 LAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEIAGLDKDKPNRVTKVAVKML 354

      KSDATEKDLSDLISEMEMMMKIGKHKNIIINLLEACTQDGPLYVIVEYASKGNLREYLQAR 487
      KSDATEKDLSDLISEMEMMMKIGKHKNIIINL ACTQDGPLYVIVEYASKGNLREYLQAR
Sbjct: 355 KSDATEKDLSDLISEMEMMMKIGKHKNIIINL GACTQDGPLYVIVEYASKGNLREYLQAR 414

      RPPGLEYCYNPSHNPEEQLSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNV 547
      RPPGLEYCYNPSHNPEEQLSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNV
Sbjct: 415 RPPGLEYCYNPSHNPEEQLSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNV 474

      MKIADFGLARDIHHIDYKKTNGRLPVKWMapeALFDRIYTHQSDVWSFGVLLWEIFTL 607
      MKIADFGLARDIHHIDYKKTNGRLPVKWMapeALFDRIYTHQSDVWSFGVLLWEIFTL
Sbjct: 475 MKIADFGLARDIHHIDYKKTNGRLPVKWMapeALFDRIYTHQSDVWSFGVLLWEIFTL 534

      GGSPPYGPVPVEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLD 667
      GGSPPYGPVPVEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVE LDR
Sbjct: 535 GGSPPYGPVPVEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDR 594

      IVALTSNQEYLDLSIPLDQYSPSPDTRSSSTCSSGSDSVFSHEPLPEEPCLPRHPTQLAN 727
      IVALTSNQEYLDLS+PLDQYSPSPDTRSSSTCSSGSDSVFSHEPLPEEPCLPRHP QLAN
Sbjct: 595 IVALTSNQEYLDLSMPLDQYSPSPDTRSSSTCSSGSDSVFSHEPLPEEPCLPRHPAQLAN 654

      SGLKRR 733
      GLKRR
Sbjct: 655 GGLKRR 660

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sp_vs  P21802-3      Isoform 3 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 822 AA
      FGFR2_HUMAN    (Human)] align

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Score = 1108 bits (2867), Expect = 0.0
Identities = 537/694 (77%), Positives = 606/694 (87%), Gaps = 7/694 (1%)

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Query: 31  DALPSSDDDDDDSSSEKETDNTKPNPVAPYWTSPPEKMEKLLHAVPAAKTVKFKCPSS 90
      DA+ S +D+DD D +      E N K  APYWT+ EKMEK+LHAVPAA TVKF+CP+
Sbjct: 126 DAISSGDEDDTDGAEDFVSENSNNKR---APYWTNTEKMEKRLHAVPAANTVCFRCPAG 182

Query: 91  GTPNPTLRWLKNGKEFKPDHRIGGYKVRVATWSIIMDSVVP SDKGNYTCIVENEYGSINH 150
      G P PT+RWLWLNKKEFK +HRIGGYKVR WS+IM+SVVPSDKGNYTC+VENEYGSINH
Sbjct: 183 GNPMPMTMRWLKNGKEFKQEHRIGGYKVRNQHWSLIMESVVP SDKGNYTCVENEYGSINH 242

Query: 151 TYQLDVVERSPhRPILQAGLPANKTVALGSNVBFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
      TY LDVVERSPhRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
Sbjct: 243 TYHLDVVERSPhRPILQAGLPANASTVVGDDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPYVQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTTRPVA 270
      PD LPY+++LKHSGINSS+AEVL LFNVT EA +GEY+CKVSNYIG+ANQSAWLTV P
Sbjct: 303 PDGLPYLKVILKHSGINSSNAEVLALFNVT EADAGEYICKVSNYIGQANQSAWLTVL-PKQ 361

Query: 271 KALEERPAMVTSPPLYLEIIYCTGAFLISCMGSGVYIYKMKSGTKKSDPHSQMAVHKLAK 330
      +A      + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TTK DF SQ AVHKL K
Sbjct: 362 QAPGREKEITASPDYLEIAIYICIGVFLIACMVVTVILCRMKN+TKKPDFSSQPAVHKLTK 421

Query: 331 SIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSG-TPMLAGVSEYELPEDPRWELPRDR 388
      IPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+
Sbjct: 422 RIPLRRQVTVSAESSSSMNSNTPLVRITTRLSSSTADTPMLAGVSEYELPEDPKWEFPDRK 481

Query: 389 LVLGKPLGEGCFGQVVLAEIAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKM 448
      L LGKPLGEGCFGQVV+AEA+G+DKDKP VAVKMLK DATEKDLSDL+SEMEMMKM
Sbjct: 482 LTLGKPLGEGCFGQVVMABAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMMKM 541

Query: 449 IGKHKNIIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPEEQLS 508
      IGKHKNIIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++
Sbjct: 542 IGKHKNIIINLLGACTQDGPLYVIVEYASKGNLREYLRRARRPPGMEYSYDINRVPEEQMTF 601

Query: 509 KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGLARDIHHIDYKKT 568
      KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NVMKIADFGLARDI++IDYKKT
Sbjct: 602 KDLVSCTYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFGLARDINNIDYKKT 661

Query: 569 TNGRLPVKWMapeALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYGPVPVEELFKLLKEGH 628
      TNGRLPVKWMapeALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYGP+PVEELFKLLKEGH
Sbjct: 662 TNGRLPVKWMapeALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYGP+PVEELFKLLKEGH 721

Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQYS 688
      RMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+EYLDLS PL+QYS
Sbjct: 722 RMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTNEEYLDLSQPLEQYS 781

Query: 689 PSFPDTRSSSTCSSGSDSVFSHEPLPEEPCLPRHP 722
      PS+PDTRSS CSSG+DSVFS +P+P EPCLP++P
Sbjct: 782 PSYPDTRSS-CSSGDSVFSPPMPYEPCLPQYP 814

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sp\_vs P21802-18 Isoform 18 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens] 820 AA  
 FGFR2\_HUMAN (Human)] align

Score = 1100 bits (2845), Expect = 0.0  
 Identities = 535/694 (77%), Positives = 604/694 (87%), Gaps = 9/694 (1%)

Query: 31 DALPSSDDDDDDSSSEKETDNTKPNPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSS 90  
 DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+  
 Sbjct: 126 DAISSGDEDDTDGAEDFVSENSNNKR--APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182

Query: 91 GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSINH 150  
 G P PT+RWLKNGKEFK +HRIGGYKVR WS+IM+SVVP SDKGNYTC+VENEYGSINH  
 Sbjct: 183 GNPMPTRWLKNGKEFKQEHRIIGGYKVRNQHWSLIMESVVP SDKGNYTCV VENEYGSINH 242

Query: 151 TYQLDVVERSPhRPILQAGLPANKTVALGNSVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210  
 TY LDVVERSPhRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G  
 Sbjct: 243 TYHLDVVERSPhRPILQAGLPANASTVVGDDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPYVQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTREPVA 270  
 PD LPY+++LKHSGINSS+AEVL LFNVTEA +GEY+CKVSNYIG+ANQSAWLTIV P  
 Sbjct: 303 PDGLPYLKVLLKHSGINSSNAEVLALFNVTEADAGEYICKVSNYIGQANQSAWLTIVL-PKQ 361

Query: 271 KALEERPAVMTSPPLYLEIIYCTGAFLISCM LGSVIIYKMKSGTKKSDPHSQMAVHKLAK 330  
 +A + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K  
 Sbjct: 362 QAPGREKEITASPDYLEIAIYCIGVFLIACMVVTIVLCRMKNTTKKPDFSSQPAVHKLTK 421

Query: 331 SIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPRDR 388  
 IPLRRQV SA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+  
 Sbjct: 422 RIPLRRQV--SAESSSSMNSNTPLVRITTRLSSSTADTPMLAGVSEYELPEDPKWEFPRDK 479

Query: 389 LVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKM 448  
 L LGKPLGEGCFGQVV+AEA+G+DKDKP VAVKMLK DATEKDLSDL+SEMEMMKM  
 Sbjct: 480 LTLGKPLGEGCFGQVVMABEAGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMMKM 539

Query: 449 IGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQ LSS 508  
 IGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++  
 Sbjct: 540 IGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLRRARRPPGMEYSYDINRVPEEQMTF 599

Query: 509 KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEADNVMKIADFGGLARDIHHIDYKKT 568  
 KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NVMKIADFGGLARDI++IDYKKT  
 Sbjct: 600 KDLVSCYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFGGLARDINNIDYKKT 659

Query: 569 TNGRLPVKWMPEALFDRYITHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGH 628  
 TNGRLPVKWMPEALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPG+PVEELFKLLKEGH  
 Sbjct: 660 TNGRLPVKWMPEALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKEGH 719

Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQYS 688  
 RMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+EYLDLS PL+QYS  
 Sbjct: 720 RMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTNEEYLDLSQPLEQYS 779

Query: 689 PSFPDRSSSTCSSGDSVFSHEPLPEEPCLPRHP 722  
 PS+PDTRSS CSSG+DSVFS +P+P EPCLP++P  
 Sbjct: 780 PSYPDTRSS-CSSGDSVFSPPDPMPYEPCLPQYP 812

sp P21802 Fibroblast growth factor receptor 2 precursor (EC 2.7.10.1) 821 AA  
 FGFR2\_HUMAN (FGFR-2) (Keratinocyte growth factor receptor 2) (CD332  
 antigen) [FGFR2] [Homo sapiens (Human)] align

Score = 1065 bits (2755), Expect = 0.0  
 Identities = 519/696 (74%), Positives = 592/696 (85%), Gaps = 12/696 (1%)

Query: 31 DALPSSDDDDDDSSSEKETDNTKPNPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSS 90  
 DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+  
 Sbjct: 126 DAISSGDEDDTDGAEDFVSENSNNKR--APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182

Query: 91 GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSINH 150  
 G P PT+RWLKNGKEFK +HRIGGYKVR WS+IM+SVVP SDKGNYTC+VENEYGSINH  
 Sbjct: 183 GNPMPTRWLKNGKEFKQEHRIIGGYKVRNQHWSLIMESVVP SDKGNYTCV VENEYGSINH 242

Query: 151 TYQLDVVERSPhRPILQAGLPANKTVALGNSVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210  
 TY LDVVERSPhRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G  
 Sbjct: 243 TYHLDVVERSPhRPILQAGLPANASTVVGDDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPYVQILKHSGINSSDAEVLTLF--NVTEAQSGEYVCKVSNYIGEANQSAWLTVTREP 268  
 PD LPY+++LK +G+N++D E+ L+ NVT +GEY C N IG + SAWLTIV  
 Sbjct: 303 PDGLPYLKVLAAGVNTTDKEIEVLYIRNVTTFEDAGEYTCLAGNSIGISPHSAWLTIVLPA 362

Query: 269 VAKALEERPAVMTSPPLYLEIIYCTGAFLISCM LGSVIIYKMKSGTKKSDPHSQMAVHKL 328

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      + E + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL
Sbjct: 363 PGREKE---ITASPDYLEIAIYCIGVFLIACMVVTILCRMKNNTTKKPDFSSQPAVHKL 418

Query: 329 AKSIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPR 386
      K IPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PR
Sbjct: 419 TKRIPLRRQVTVSAESSSSMNSNTPLVRITTRLSSSTADTPMLAGVSEYELPEDPKWEFPR 478

Query: 387 DRLVLGKPLGEGCGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 446
      D+L LGKPLGEGCGQVV+AEA+G+DKDKP VAVKMLK DATEKDLSDL+SEMEMM
Sbjct: 479 DKLTLGKPLGEGCGQVVMFAEAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMM 538

Query: 447 KMIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQ 506
      KMIGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ+
Sbjct: 539 KMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLRRARRPPGMEYSYDINRVPEEQM 598

Query: 507 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEENVMKIADFLGLARDIHHIDYK 566
      + KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NMVKIADFLGLARDI++IDYK
Sbjct: 599 TFKDLVSCYQLARGMEYLASQKCIHRDLAARNVLVTEENVMKIADFLGLARDINNIDYK 658

Query: 567 KTTNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVEELFKLLKE 626
      KTTNGRLPVKWMAPALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPG+PVEELFKLLKE
Sbjct: 659 KTTNGRLPVKWMAPALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKE 718

Query: 627 GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIALTSNQEYLDLSIPLDQ 686
      GHRMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+EYLDLS PL+Q
Sbjct: 719 GHRMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRIALTNTNEEYLDLSQPLEQ 778

Query: 687 YSPSFPDTRSSSTCSSGEDSVFSHEPLPEEPCLPRHP 722
      YSPS+PDTRSS CSSG+DSVFS +P+P EPCLP++P
Sbjct: 779 YSPSYPDTRSS-CSSGDDSVFSPDMPYEPCLPQYP 813

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sp_vs F21802-5      Isoform 5 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 819 AA
      FGFR2_HUMAN   (Human)] align

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Score = 1057 bits (2733), Expect = 0.0
Identities = 517/696 (74%), Positives = 590/696 (84%), Gaps = 14/696 (2%)

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Query: 31 DALPSSDEDDDDSSSEKETDNTKPNVPAPYWTSPKMEKKLHAVPAAKTVKFCPS 90
      DA+ S +D+DD D+ E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
Sbjct: 126 DAISSGDEDDTDGAEDFVSENSNNKR---APYWTNTEKMEKKLHAVPAANTVKFRCPAG 182

Query: 91 GTPNPTRLRWLKNKGEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSINH 150
      G P PT+RWLKNKGEFK +HRIGGYKVR WS+IM+SVVP SDKGNYTC+VENEYGSINH
Sbjct: 183 GNPMPTRLRWLKNKGEFKQEHRIIGGYKVRNQHWSLIMESVVP SDKGNYTCVENEYGSINH 242

Query: 151 TYQLDVVERSHPHPIQLAGLPANKTVALGSNVFEMCKVYSDPQPHIQWLKHIEVNGSKIG 210
      TY LDVVERSHPHPIQLAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
Sbjct: 243 TYHLDVVERSHPHPIQLAGLPANASTVVGDDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPPYQILKHSGINSSDAEVLTLF--NVTEAQSGEYVCKVSNYIGEANQSAWLTVTRP 268
      PD LPY+++LK +G+N++D E+ L+ NVT +GEY C N IG + SAWLTV
Sbjct: 303 PDGLPYLKVLAAGVNTTDKEIEVLVIRNVT FEDAGEYTCLAGNSIGISPHSAWLTVLPA 362

Query: 269 VAKALEERPAVMTSPYLEIIIIYCTGAPLISCMLGSVIIYKMKSGTKKSDPHSQMAVHKL 328
      + E + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL
Sbjct: 363 PGREKE---ITASPDYLEIAIYCIGVFLIACMVVTILCRMKNNTTKKPDFSSQPAVHKL 418

Query: 329 AKSIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPR 386
      K IPLRRQV SA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PR
Sbjct: 419 TKRIPLRRQV--SAESSSMNSNTPLVRITTRLSSSTADTPMLAGVSEYELPEDPKWEFPR 476

Query: 387 DRLVLGKPLGEGCGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 446
      D+L LGKPLGEGCGQVV+AEA+G+DKDKP VAVKMLK DATEKDLSDL+SEMEMM
Sbjct: 477 DKLTLGKPLGEGCGQVVMFAEAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMM 536

Query: 447 KMIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQ 506
      KMIGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ+
Sbjct: 537 KMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLRRARRPPGMEYSYDINRVPEEQM 596

Query: 507 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEENVMKIADFLGLARDIHHIDYK 566
      + KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NMVKIADFLGLARDI++IDYK
Sbjct: 597 TFKDLVSCYQLARGMEYLASQKCIHRDLAARNVLVTEENVMKIADFLGLARDINNIDYK 656

Query: 567 KTTNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVEELFKLLKE 626
      KTTNGRLPVKWMAPALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPG+PVEELFKLLKE
Sbjct: 657 KTTNGRLPVKWMAPALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKE 716

Query: 627 GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIALTSNQEYLDLSIPLDQ 686
      GHRMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+EYLDLS PL+Q
Sbjct: 717 GHRMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRIALTNTNEEYLDLSQPLEQ 776

Query: 687 YSPSFPDTRSSSTCSSGEDSVFSHEPLPEEPCLPRHP 722
      YSPS+PDTRSS CSSG+DSVFS +P+P EPCLP++P
Sbjct: 777 YSPSYPDTRSS-CSSGDDSVFSPDMPYEPCLPQYP 811

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sp\_vs P21802-16 Isoform 16 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 822 AA  
FGFR2\_HUMAN (Human)] align

Score = 1051 bits (2719), Expect = 0.0  
Identities = 517/699 (73%), Positives = 590/699 (84%), Gaps = 17/699 (2%)

Query: 31 DALPSSDDDDDDSSSEKETDNTKPNPVAPYWTSPKMEKKLHAVPAAKTVKFKCPSS 90  
DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+  
Sbjct: 126 DAISSGDEDDTDGAEDFVSENSNNKR--APYWTNTEKMEKKLHAVPAANTVKFRCPAG 182

Query: 91 GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSPDKGNYTCIVENEYGSINH 150  
G P PT+RWLKNGKEFK +HRIGGYKVR WS+IM+SVVPSPDKGNYTC+VENEYGSINH  
Sbjct: 183 GNPMPTRWLKNGKEFKQEHRRIGGYKVRNQHWSLIMESVVPSPDKGNYTCVENEYGSINH 242

Query: 151 TYQLDVVERSPhRPILQAGLPANKTVALGNSNVEFMCKVSDPQPHIQWLKHIEVNGSKIG 210  
TY LDVVERSPhRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G  
Sbjct: 243 TYHLDVVERSPhRPILQAGLPANASTVVGSDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPPYQILK---HSGINSSDAEVLTLF--NVTEAQSGEYVCKVSNYIGEANQSAWLTV 265  
PD LPY++LK +G+N++D E+ L+ NVT +GEY C N IG + SAWLTV  
Sbjct: 303 PDGLPYLKVLLKAAAGVNTTDKIEVLYIRNVTPEADAGEYTCLAGNSIGISFHSWLTV 362

Query: 266 TRPVAKALEERPAMVTSPLYLEIIYCTGAPLISCMGSLVYIYKMKSGTKKSDPHSQMAV 325  
+ E + SP YLEI IYC G PLI+CM+ +VI+ +MK+ TKK DF SQ AV  
Sbjct: 363 LPAPGREKE---ITASPDYLEIAIYICIGVPLIACMVVTILCRMKNNTTKKPDFSSQPAV 418

Query: 326 HKLAKSIPLRRQVTSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWE 383  
HKL K IPLRRQV SA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE  
Sbjct: 419 HKLTKRIPLRRQV--SAESSSMNSNTPLVRITTRLSTADTPMLAGVSEYELPEDPKWE 476

Query: 384 LPRDRLVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEM 443  
PRD+L LGKPLGEGCFGQVV+AEA+G+DKDKP VAVKMLK DATEKDLSDL+SEM  
Sbjct: 477 FPRDKITLGLKPLGEGCFGQVVMABAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEM 536

Query: 444 EMMKMIGKHKNIINLLEACTQDGLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPE 503  
EMMKMIGKHKNIINLL ACTQDGLYVIVEYASKGNLREYL+ARRPFG+EY Y+ + PE  
Sbjct: 537 EMMKMIGKHKNIINLLGACTQDGLYVIVEYASKGNLREYLARRPPGMEYSYDINRVPE 596

Query: 504 EQLSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEENVMKIADPGLARDIHID 563  
EQ++ KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NVMKIADPGLARDI++ID  
Sbjct: 597 EQMTFKDLVSCYQLARGMEYLASQKCIHRDLAARNVLVTEENVMKIADPGLARDIINID 656

Query: 564 YYKKTNGRLPVKWMAPALFDRYTHQSDVWSFGVLLWEIFTLGGSPYPGPVEELFKL 623  
YYKKTNGRLPVKWMAPALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPGP+PVEELFKL  
Sbjct: 657 YYKKTNGRLPVKWMAPALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGPVVEELFKL 716

Query: 624 LKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTNSQEYLDLSIP 683  
LKEGHRMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+EYLDLS P  
Sbjct: 717 LKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTNEEYLDLSQP 776

Query: 684 LDQYSPSPDTRSSSTCSSGDSVFSHEPLPEEPCLPRHP 722  
L+QYSPS+PDTRSS CSSG+DSVFS +P+P EPCLP++P  
Sbjct: 777 LEQYSPSPDTRSS-CSSGDSVFSPPDMPYEPCLPQYP 814

sp\_vs P21802-20 Isoform 20 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 704 AA  
FGFR2\_HUMAN (Human)] align

Score = 1046 bits (2706), Expect = 0.0  
Identities = 520/726 (71%), Positives = 593/726 (81%), Gaps = 34/726 (4%)

Query: 1 MWGKCLLWAVLVATLCTARPAPTLPQDALPSSDDDDDDSSSEKETDNTKPNPV 60  
M W + V+ ATL ARP+ +L E D T  
Sbjct: 1 MVSWGRFICLVVVTMATLSLARPFSFLVE-----DTTLEPEG 37

Query: 61 APYWTSPKMEKKLHAVPAAKTVKFKCPSSSGTFNPTLRWLKNGKEFKPDHRIGGYKVRYA 120  
APYWT+ EKMEK+LHAVPAA TVKF+CP+ G P PT+RWLKNGKEFK +HRIGGYKVR  
Sbjct: 38 APYWTNTEKMEKKLHAVPAANTVKFRCPAGGNPMPTRWLKNGKEFKQEHRRIGGYKVRNQ 97

Query: 121 TWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQLDVVERSPhRPILQAGLPANKTVALGS 180  
WS+IM+SVVPSPDKGNYTC+VENEYGSINHTY LDVVERSPhRPILQAGLPAN + +G  
Sbjct: 98 HWSLIMESVVPSPDKGNYTCVENEYGSINHTYHLDVVERSPhRPILQAGLPANASTVVG 157

Query: 181 NVEFMCKVSDPQPHIQWLKHIEVNGSKIGPDNLPPYQILKHSGINSSDAEVLTLF--NV 238  
+VEF+CKVYSD QPHIQW+KH+E NGSK GPD LPY++LK +G+N++D E+ L+ NV  
Sbjct: 158 DVEFVCKVYSDAQPHIQWIKHVEKNGSKYGPDLPLKVLKAAAGVNTTDKIEVLYIRNV 217

Query: 239 TEAQSGEYVCKVSNYIGEANQSAWLTVTRPVAKALEERPAMVTSPLYLEIIYCTGAPLI 298  
T +GEY C N IG + SAWLTV + E + SP YLEI IYC G FLI

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Sbjct: 218 TFDAGEYTCLAGNSIGISFHSAWLTVLPAPGREKE---ITASPDYLEIAIYCIGVFLI 273
Query: 299 SCMLGSVIIYKMKSGTKKSDPHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVR-P 357
      +CM+ +VI+ +MK+ TKK DF SQ AVHKL K IPLRRQV SA+SS+SMNS LVR
Sbjct: 274 ACMVVTVILCRMKNNTTKPDFSSQFAVHKLTKRIPLRQV--SAESSSSMNSNTPLVRIT 331
Query: 358 SRLSSSG-TPMLAGVSEYELPEDPRWELPRDRVLGKPLGEGCFGQVVLAAEIGLDKDKP 416
      +RLSS+ TPMLAGVSEYELPEDP+WE PRD+L LGKPLGEGCFGQVV+AEA+G+DKDKP
Sbjct: 332 TRLSSTADTPMLAGVSEYELPEDPKWEFPRDKLTGKPLGEGCFGQVVMAEAVGIDKDKP 391
Query: 417 NRVTKVAVKMLKSDATEKDLSDLISEMEMMMKIGKHNIINLLEACTQDGPLYVIVEYAS 476
      VAVKMLK DATEKDLSDL+SEMEMMMKIGKHNIINLL ACTQDGPLYVIVEYAS
Sbjct: 392 KEAVTVAVKMLKDDATEKDLSDLVSEMEMMMKIGKHNIINLLGACTQDGPLYVIVEYAS 451
Query: 477 KGNLREYLQARRPPGLECYNPSHNPEEQQLSSKDLVSCAYQVARGMEYLASKKCIHRDLA 536
      KGNLREYL+ARRPPG+EY Y+ + PEEQ++ KDLVSC YQ+ARGMEYLAS+KCIHRDLA
Sbjct: 452 KGNLREYLRARRPPGMEYSYDINRVPEEQMTFKDLVSCYQLARGMEYLASQKCIHRDLA 511
Query: 537 ARNVLVTEEDNVMKIADFGGLARDIHHIDYKKTTNGRLPVKWMPEALFDRYTHQSDVWS 596
      ARNVLVTE+NVMKIADFGGLARDI++IDYKKTTNGRLPVKWMPEALFDR+YTHQSDVWS
Sbjct: 512 ARNVLVTEEDNVMKIADFGGLARDINNIDYKKTTNGRLPVKWMPEALFDRVYTHQSDVWS 571
Query: 597 FGVLLWEIFTLGGSPYPGVPVEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRP 656
      FGVL+WEIFTLGGSPYPG+PVEELFKLLKEGHRMDKP+NCTNELYMMMRDCWHAVPSQRP
Sbjct: 572 FGVLMWEIFTLGGSPYPGIPVEELFKLLKEGHRMDKPANCTNELYMMMRDCWHAVPSQRP 631
Query: 657 TFKQLVEVLDRIVALTSNQEYLDLSIPLDQYSPSPDTRSSCTSSGSDSVFSHEPLPEEP 716
      TFKQLVE LDRI+ LT+N+EYLDLS PL+QYSPS+PDTRSS CSSG+DSVFS +P+P EP
Sbjct: 632 TFKQLVEDLDRILTLTNEEYLDLSQPLEQYSPSPDTRSS--CSSGSDSVFSPDMPPEP 690
Query: 717 CLPRHP 722
      CLP++P
Sbjct: 691 CLPQYP 696

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sp\_vs P21802-7 Isoform 7 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 817 AA  
 FGFR2\_HUMAN (Human)] align

Score = 1040 bits (2688), Expect = 0.0  
 Identities = 507/674 (75%), Positives = 571/674 (84%), Gaps = 6/674 (0%)

```

Query: 31 DALPSSDDDDDDSSSEKETDNTKPNPVAPYWTSPKMEKKLHAVPAAKTVKFKCPSS 90
      DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
Sbjct: 126 DAISSGDDDDTDGAEDFVSENSNNKR--APYWTNTEKMEKRLHAVPAAANTVKFRCPAG 182
Query: 91 GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSINH 150
      G P PT+RWLKNGKEFK +HRIGGYKVR WS+IM+SVVPSDKGNYTC+VENEYGSINH
Sbjct: 183 GNPMPTRMWLKNGKEFKQEHRIIGGYKVRNQHWSLIMESVVP SDKGNYTCVVENEYGSINH 242
Query: 151 TYQLDVVERSPhRPILQAGLPANKTVALGNSVEFMCKVSDPQPHIQWLKHIEVNGSKIG 210
      TY LDVVERSPhRPILQAGLPAN + +G +VEF+CKVYS D QPHIQW+KH+E NGSK G
Sbjct: 243 TYHLDVVERSPhRPILQAGLPANASTVVG DVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302
Query: 211 PDNLPPYQILKHSNGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVA 270
      PD LPY+++LKHSNGINSS+AEVL LFNVT EA +GEY+CKVSNYIG+ANQSAWLT V P
Sbjct: 303 PDGLPYLKV LKHSNGINSSNAEVLALFNVT EADAGEYICKVSNYIGANQSAWLTVL-PKQ 361
Query: 271 KALEERPAVMTSPLYLEIIYCTGAFLISCMGLSVIIYKMKSGTKKSDPHSQMAVHKLAK 330
      +A + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K
Sbjct: 362 QAPGREKEITASPDYLEIAIYCIGVFLIACMVVTVILCRMKNNTTKPDFSSQFAVHKLT 421
Query: 331 SIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPRDR 388
      IPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+
Sbjct: 422 RIPLRRQVTVSAESSSSMNSNTPLVRITRLSSTADTPMLAGVSEYELPEDPKWEFPRDK 481
Query: 389 LVLGKPLGEGCFGQVVLAAEIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMMK 448
      L LGKPLGEGCFGQVV+AEA+G+DKDKP VAVKMLK DATEKDLSDL+SEMEMMMK
Sbjct: 482 LTLGKPLGEGCFGQVVM AEAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMMMK 541
Query: 449 IGKHKNIIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQQLSS 508
      IGKHKNIIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++
Sbjct: 542 IGKHKNIIINLLGACTQDGPLYVIVEYASKGNLREYLRARRPPGMEYSYDINRVPEEQMTF 601
Query: 509 KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEEDNVMKIADFGGLARDIHHIDYKKT 568
      KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NVMKIADFGGLARDI++IDYKKT
Sbjct: 602 KDLVSCYQLARGMEYLASQKCIHRDLAARNVLVTEENNVMKIADFGGLARDINNIDYKKT 661
Query: 569 TNGRLPVKWMPEALFDRYTHQSDVWSFGVLLWEIFTLGGSPYPGVPVEELFKLLKEGH 628
      TNGRLPVKWMPEALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPG+PVEELFKLLKEGH
Sbjct: 662 TNGRLPVKWMPEALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKEGH 721
Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPFTFKQLVEVLDRIVALTSNQEYLDLSIPLDQYS 688
      RMDKP+NCTNELYMMMRDCWHAVPSQRPFTFKQLVE LDRI+ LT+N+ Y L P
Sbjct: 722 RMDKPANCTNELYMMMRDCWHAVPSQRPFTFKQLVEDLDRILTLTNERYKLLPCFDKHNK 781

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Query: 689 PSFPDTRSSSTCSSG 702  
 P+ R +G  
 Sbjct: 782 RCKPEERGDLEAG 795

sp\_vs P21802-9 Isoform 9 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 819 AA  
 FGFR2\_HUMAN (Human)] align

Score = 1036 bits (2680), Expect = 0.0  
 Identities = 503/653 (77%), Positives = 566/653 (86%), Gaps = 6/653 (0%)

Query: 31 DALPSSSEDDDDDDSSSEKETDNTKPNPVAPYWTSPPEKMEKKLHAVPAAKTVKFKCPSS 90  
 DA+ S +D+DD D+ E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+  
 Sbjct: 126 DAISGGDEDDTDGAEDFVSENSNNKR---APYWTNTEKMEKRLHAVPAANTVKFRCPCAG 182

Query: 91 GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSINH 150  
 G P PT+RWLKNGKEFK +HRIGGYKVR WS+IM+SVVPSDKGNYTC+VENEYGSINH  
 Sbjct: 183 GNPMPTRWLKNGKEFKQEHRIIGGYKVRNQHWSLIMESVVP SDKGNYTCVENEYGSINH 242

Query: 151 TYQLDVVERSPhRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210  
 TY LDVVERSPhRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G  
 Sbjct: 243 TYHLDVVERSPhRPILQAGLPANASTVVGDDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPPYVQILKHSNGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVA 270  
 PD LPY+++LKHSGINSS+AEVL LFNVTQA +GEY+CKVSNYIG+ANQSAWLTV P  
 Sbjct: 303 PDGLPYLKLKHSNGINSSNAEVLALFNVTQAAGEYICKVSNYIGQANQSAWLTVL-PKQ 361

Query: 271 KALEERPAVMTSPYLEIIYCTGAFLISCMGSLVYIYKMKSGTKKSDPHSQMAVHKLAK 330  
 +A + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K  
 Sbjct: 362 QAPGREKEITASPDYLEIAIYICIGVFLIACMVVTVILCRMKNNTTKKPDFSSQPAVHKLTK 421

Query: 331 SIPLRRQVTVSADSSASMNNGSVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPRDR 388  
 IPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+  
 Sbjct: 422 RIPLRRQVTVSAESSSSMNNTPLVRITRLSSSTADTPMLAGVSEYELPEDPKWEFFPRDK 481

Query: 389 LVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKM 448  
 L LGKPLGEGCFGQVV+AEA+G+DKDKP VAVKMLK DATEKDLSDL+SEMEMMKM  
 Sbjct: 482 LTLGKPLGEGCFGQVVMABAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMMKM 541

Query: 449 IGKHKNIINLLEACTQDGLPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQQLSS 508  
 IGKHKNIINLL ACTQDGLPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++  
 Sbjct: 542 IGKHKNIINLLGACTQDGLPLYVIVEYASKGNLREYLRRARRPPGMEYSYDINRVPEEQMTF 601

Query: 509 KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGLARDIHHIDYYKKT 568  
 KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NVMKIADFGLARDI++IDYYKKT  
 Sbjct: 602 KDLVSCYQVQLARGMEYLASKKCIHRDLAARNVLVTENNVMKIADFGLARDINNIDYYKKT 661

Query: 569 TNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELPKLLKEGH 628  
 TNGRLPVKWMAPALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPG+PVEELPKLLKEGH  
 Sbjct: 662 TNGRLPVKWMAPALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGPVVEELPKLLKEGH 721

Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLS 681  
 RMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+ L L+  
 Sbjct: 722 RMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTITNERILTLT 774

sp\_vs P21802-10 Isoform 10 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 819 AA  
 FGFR2\_HUMAN (Human)] align

Score = 1035 bits (2676), Expect = 0.0  
 Identities = 501/649 (77%), Positives = 564/649 (86%), Gaps = 6/649 (0%)

Query: 31 DALPSSSEDDDDDDSSSEKETDNTKPNPVAPYWTSPPEKMEKKLHAVPAAKTVKFKCPSS 90  
 DA+ S +D+DD D+ E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+  
 Sbjct: 126 DAISGGDEDDTDGAEDFVSENSNNKR---APYWTNTEKMEKRLHAVPAANTVKFRCPCAG 182

Query: 91 GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSINH 150  
 G P PT+RWLKNGKEFK +HRIGGYKVR WS+IM+SVVPSDKGNYTC+VENEYGSINH  
 Sbjct: 183 GNPMPTRWLKNGKEFKQEHRIIGGYKVRNQHWSLIMESVVP SDKGNYTCVENEYGSINH 242

Query: 151 TYQLDVVERSPhRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210  
 TY LDVVERSPhRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G  
 Sbjct: 243 TYHLDVVERSPhRPILQAGLPANASTVVGDDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPPYVQILKHSNGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVA 270  
 PD LPY+++LKHSGINSS+AEVL LFNVTQA +GEY+CKVSNYIG+ANQSAWLTV P  
 Sbjct: 303 PDGLPYLKLKHSNGINSSNAEVLALFNVTQAAGEYICKVSNYIGQANQSAWLTVL-PKQ 361

Query: 271 KALEERPAVMTSPYLEIIYCTGAFLISCMGSLVYIYKMKSGTKKSDPHSQMAVHKLAK 330  
 +A + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K  
 Sbjct: 362 QAPGREKEITASPDYLEIAIYICIGVFLIACMVVTVILCRMKNNTTKKPDFSSQPAVHKLTK 421

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Query: 331 SIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPRDR 388
      IPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+
Sbjct: 422 RIPLRRQVTVSAESSSSMNSNTPLVRITRLSSTADTPMLAGVSEYELPEDPKWEPRDK 481

Query: 389 LVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKM 448
      L LGKPLGEGCFGQVV+AEA+G+DKDKP VAVKMLK DATEKDLSDL+SEMEMMKM
Sbjct: 482 LTLGKPLGEGCFGQVVMABAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMMKM 541

Query: 449 IGKHKNINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQQLSS 508
      IGKHKNINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++
Sbjct: 542 IGKHKNINLLGACTQDGPLYVIVEYASKGNLREYLRRARRPPGMEYSYDINRVPEEQMTF 601

Query: 509 KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTE+NMVKIADFGGLARDIHHIDYYKKT 568
      KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NMVKIADFGGLARDI++IDYYKKT
Sbjct: 602 KDLVSCYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFGGLARDINNIDYYKKT 661

Query: 569 TNGRLPVKWMMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGH 628
      TNGRLPVKWMMAPEALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPG+PVEELFKLLKEGH
Sbjct: 662 TNGRLPVKWMMAPEALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGPVVEELFKLLKEGH 721

Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQ 677
      RMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+ +
Sbjct: 722 RMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTTNESF 770

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sp\_vs P21802-11 Isoform 11 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 830 AA  
FGFR2\_HUMAN (Human)] align

Score = 1034 bits (2673), Expect = 0.0  
Identities = 501/647 (77%), Positives = 563/647 (87%), Gaps = 6/647 (0%)

```

Query: 31 DALPSSDDDDDDSSSEKEKTDNTKPNPVAPYWTSPKMEKKLHAVPAAKTVKFKCPSS 90
      DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
Sbjct: 126 DAISSGDDEDDTDGAEDFVSENSNNKR---APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182

Query: 91 GTPNPTLRWLKNGKEFKPDHRIGGYKVRVATWSIIMDSVVP SDKGNYTCIVENEYGSINH 150
      G P PT+RWLKNGKEFK +HRIGGYKVR WS+IM+SVVP SDKGNYTC+VENEYGSINH
Sbjct: 183 GNPMPTRWRLKNGKEFKQEHRIIGGYKVRNQHWSLIMESVVP SDKGNYTCVENEYGSINH 242

Query: 151 TYQLDVVERSPhRPILQAGLPANKTVALGNSNVEFMCKVYSDQPQHIQWLKHIEVNGSKIG 210
      TY LDVVERSPhRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
Sbjct: 243 TYHLDVVERSPhRPILQAGLPANASTVVGDDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPYVQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVA 270
      PD LPY+++LKHSGINSS+AEVL LFNVTEA +GEY+CKVSNYIG+ANQSAWLTV P
Sbjct: 303 PDGLPYLKVILKHSGINSSNAEVLALFNVTEADAGEYICKVSNYIGQANQSAWLTVL-PKQ 361

Query: 271 KALEERPAVMTSPPLYLEIIYCTGAFLISCMLGSVIIYKMSGTTKSDFHQSMAVHKLAK 330
      +A + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K
Sbjct: 362 QAPGREKEITASPDYLEIAIYCIYGVFLIACMVVTILCRMKNNTTKKPDFSSQPAVHKLTK 421

Query: 331 SIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPRDR 388
      IPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+
Sbjct: 422 RIPLRRQVTVSAESSSSMNSNTPLVRITRLSSTADTPMLAGVSEYELPEDPKWEPRDK 481

Query: 389 LVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKM 448
      L LGKPLGEGCFGQVV+AEA+G+DKDKP VAVKMLK DATEKDLSDL+SEMEMMKM
Sbjct: 482 LTLGKPLGEGCFGQVVMABAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMMKM 541

Query: 449 IGKHKNINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQQLSS 508
      IGKHKNINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++
Sbjct: 542 IGKHKNINLLGACTQDGPLYVIVEYASKGNLREYLRRARRPPGMEYSYDINRVPEEQMTF 601

Query: 509 KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTE+NMVKIADFGGLARDIHHIDYYKKT 568
      KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NMVKIADFGGLARDI++IDYYKKT
Sbjct: 602 KDLVSCYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFGGLARDINNIDYYKKT 661

Query: 569 TNGRLPVKWMMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGH 628
      TNGRLPVKWMMAPEALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPG+PVEELFKLLKEGH
Sbjct: 662 TNGRLPVKWMMAPEALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGPVVEELFKLLKEGH 721

Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQ 675
      RMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+
Sbjct: 722 RMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTTNE 768

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sp\_vs P21802-12 Isoform 12 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 771 AA  
FGFR2\_HUMAN (Human)] align



Score = 1034 bits (2673), Expect = 0.0  
Identities = 501/647 (77%), Positives = 563/647 (87%), Gaps = 6/647 (0%)

```

Query: 31  DALPSSDDDDDDSSSEKETDNTKPNVPAPYWTSPKMEKKLHAVPAAKTVKFKCPSS 90
          DA+ S +D+DD D +      E N K   APYWT+ EKMEK+LHAVPAA TVKF+CP+
Sbjct: 126 DAISSGDEDDDDTDGAEDFVSENSNNKR-- -APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182

Query: 91  GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSPDKGNYTCIVENEYGSINH 150
          G P PT+RWLNGKEFK +HRIGGYKVR  WS+IM+SVVPSDKGNYTC+VENEYGSINH
Sbjct: 183 GNPMPTRMWLNGKEFKQEHRIGGYKVRNQHWSLIMESVVPSPDKGNYTCVENEYGSINH 242

Query: 151 TYQLDVVERSPhRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
          TY LDVVERSPhRPILQAGLPAN +   +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
Sbjct: 243 TYHLDVVERSPhRPILQAGLPANASTTVVGGDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPYVQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVA 270
          PD LPY+++LKHSGINSS+AEVL LFNVTEA +GEY+CKVSNYIG+ANQSAWLTV P
Sbjct: 303 PDGLPYLKVLKHSGINSSNAEVLALFNVTEADAGEYICKVSNYIGQANQSAWLTVL-PKQ 361

Query: 271 KALEERPAVMTSPPLYLEIIYCTGAFLISCMLGSVIIYKMKSGTKKSDPHSQMAVHKLAK 330
          +A      + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K
Sbjct: 362 QAPGREKEITASPDYLEIAIYCIGVFLIACMVVTILCRMKNNTKKPDFSSQPAVHKLTK 421

Query: 331 SIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPRDR 388
          IPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+
Sbjct: 422 RIPLRRQVTVSAESSSSMNSNTPLVRITRLSSTADTPMLAGVSEYELPEDPKWEFPRDK 481

Query: 389 LVLGKPLGEGCFGQVVLAEAGLKDCKPNRVTKVAVKMLKSDATEKDLSLISEMEMMKM 448
          L LGKPLGEGCFGQV+AEA+G+DKDKP VAVKMLK DATEKDLSL+SEMEMMKM
Sbjct: 482 LTLGKPLGEGCFGQVVMAEAVGIDKDKPKEAVTVAVKMLKDDATEKDLSLSEMEMMKM 541

Query: 449 IGKHKNIINLLEACTQDGLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQQLSS 508
          IGKHKNIINLL ACTQDGLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++
Sbjct: 542 IGKHKNIINLLGACTQDGLYVIVEYASKGNLREYLRRARRPPGMEYSYDINRVPEEQMTF 601

Query: 509 KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGGLARDIHHIDYKKT 568
          KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NVMKIADFGGLARDI+IDYKKT
Sbjct: 602 KDLVSCYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFGGLARDINNIDYKKT 661

Query: 569 TNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGH 628
          TNGRLPVKWMAPALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPG+PVEELFKLLKEGH
Sbjct: 662 TNGRLPVKWMAPALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKEGH 721

Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQ 675
          RMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+
Sbjct: 722 RMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTTNE 768

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sp\_vs P21802-13 Isoform 13 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 768 AA  
FGFR2\_HUMAN (Human)] align

Score = 1034 bits (2673), Expect = 0.0  
Identities = 501/647 (77%), Positives = 563/647 (87%), Gaps = 6/647 (0%)

```

Query: 31  DALPSSDDDDDDSSSEKETDNTKPNVPAPYWTSPKMEKKLHAVPAAKTVKFKCPSS 90
          DA+ S +D+DD D +      E N K   APYWT+ EKMEK+LHAVPAA TVKF+CP+
Sbjct: 126 DAISSGDEDDDDTDGAEDFVSENSNNKR-- -APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182

Query: 91  GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSPDKGNYTCIVENEYGSINH 150
          G P PT+RWLNGKEFK +HRIGGYKVR  WS+IM+SVVPSDKGNYTC+VENEYGSINH
Sbjct: 183 GNPMPTRMWLNGKEFKQEHRIGGYKVRNQHWSLIMESVVPSPDKGNYTCVENEYGSINH 242

Query: 151 TYQLDVVERSPhRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
          TY LDVVERSPhRPILQAGLPAN +   +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
Sbjct: 243 TYHLDVVERSPhRPILQAGLPANASTTVVGGDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPYVQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVA 270
          PD LPY+++LKHSGINSS+AEVL LFNVTEA +GEY+CKVSNYIG+ANQSAWLTV P
Sbjct: 303 PDGLPYLKVLKHSGINSSNAEVLALFNVTEADAGEYICKVSNYIGQANQSAWLTVL-PKQ 361

Query: 271 KALEERPAVMTSPPLYLEIIYCTGAFLISCMLGSVIIYKMKSGTKKSDPHSQMAVHKLAK 330
          +A      + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K
Sbjct: 362 QAPGREKEITASPDYLEIAIYCIGVFLIACMVVTILCRMKNNTKKPDFSSQPAVHKLTK 421

Query: 331 SIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPRDR 388
          IPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+
Sbjct: 422 RIPLRRQVTVSAESSSSMNSNTPLVRITRLSSTADTPMLAGVSEYELPEDPKWEFPRDK 481

Query: 389 LVLGKPLGEGCFGQVVLAEAGLKDCKPNRVTKVAVKMLKSDATEKDLSLISEMEMMKM 448
          L LGKPLGEGCFGQV+AEA+G+DKDKP VAVKMLK DATEKDLSL+SEMEMMKM
Sbjct: 482 LTLGKPLGEGCFGQVVMAEAVGIDKDKPKEAVTVAVKMLKDDATEKDLSLSEMEMMKM 541

Query: 449 IGKHKNIINLLEACTQDGLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQQLSS 508
          IGKHKNIINLL ACTQDGLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++

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```

Sbjct: 542 IGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLRRARRPPGMEYSYDINRVPEEQMTF 601
Query: 509 KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEEDNVMKIADFGGLARDIHHIDYKKT 568
          KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NVMKIADFGGLARDI++IDYKKT
Sbjct: 602 KDLVSCITYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFGGLARDINNIDYKKT 661
Query: 569 TNGRLPVKWMapeALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGH 628
          TNGRLPVKWMapeALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPG+PVEELFKLLKEGH
Sbjct: 662 TNGRLPVKWMapeALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKEGH 721
Query: 629 RMDKPSNCTNELYMMMRDCWHA VPSQRPTFKQLVEVLDRIVALTSNQ 675
          RMDKP+NCTNELYMMMRDCWHA VPSQRPTFKQLVE LDRI+ LT+N+
Sbjct: 722 RMDKPANCTNELYMMMRDCWHA VPSQRPTFKQLVEDLDRILTLTTNE 768

```

sp\_vs P21802-17 Isoform 17 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 769 AA  
FGFR2\_HUMAN (Human)] align

Score = 1034 bits (2673), Expect = 0.0  
Identities = 501/647 (77%), Positives = 563/647 (87%), Gaps = 6/647 (0%)

```

Query: 31 DALPSSDDDDDDSSSEKETDNTKPNPVAPYWTSPKMEKKLHAVPAAKTVKFKCPSS 90
          DA+ S +D+DD D+ E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
Sbjct: 126 DAISSGDEDDDTGAEDFVSENSNNKR---APYWTNTEKMEKKRLHAVPAANTVKFRCPAG 182
Query: 91 GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGN YTCIVENEYGSINH 150
          G P PT+RWLKNGKEFK +HRIGGYKVR WS+IM+SVVP SDKGN YTC+VENEYGSINH
Sbjct: 183 GNPMPMTMRWLKNGKEFKQEHRRIGGYKVRNQHWSLIMESVVP SDKGN YTCV VENEYGSINH 242
Query: 151 TYQLDVVERSPhRPILQAGLPANKTVALGNSVVEFMCKVSDPQPHIQWLKHIEVNGSKIG 210
          TY LDVVERSPhRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
Sbjct: 243 TYHLDVVERSPhRPILQAGLPANASTVVGGDVEFVCKVYSDA QPHIQWIKHVEKNGSKYG 302
Query: 211 PDNLPHYQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVA 270
          PD LPY+++LKHSGINSS+AEVL LFNVTEA +GEY+CKVSNYIG+ANQSAWLTV P
Sbjct: 303 PDGLPYLKV LKHSGINSSNAEVL LFNVTEADAGEYICKVSNYIGQANQSAWLTVL-PKQ 361
Query: 271 KALEERPAVMTSPLYLEIIYCTGAFLISCM LGSVIIYKMKSGTKKSDPHSQMAVHKLAK 330
          +A + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K
Sbjct: 362 QAPGREKEITASPDYLEIAIYCI GVFLIACMVVTILCRMKN TTKKPDFSSQPAVHKLTK 421
Query: 331 SIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPLAGVSEYELPEDPRWELPRDR 388
          IPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+
Sbjct: 422 RIPLRRQVTVSADSSSMNSNTPLVRITRLSTADTPMLAGVSEYELPEDPKWEFPRDK 481
Query: 389 LVLGKPLGEGCFGQVVLA EAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKM 448
          L LGKPLGEGCFGQVV+AEA+G+DKDKP VAVKMLK DATEKDLSDL+SEMEMMKM
Sbjct: 482 LTLGKPLGEGCFGQVVM AEAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMMKM 541
Query: 449 IGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQLS 508
          IGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++
Sbjct: 542 IGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLRRARRPPGMEYSYDINRVPEEQMTF 601
Query: 509 KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEEDNVMKIADFGGLARDIHHIDYKKT 568
          KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NVMKIADFGGLARDI++IDYKKT
Sbjct: 602 KDLVSCITYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFGGLARDINNIDYKKT 661
Query: 569 TNGRLPVKWMapeALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGH 628
          TNGRLPVKWMapeALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPG+PVEELFKLLKEGH
Sbjct: 662 TNGRLPVKWMapeALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKEGH 721
Query: 629 RMDKPSNCTNELYMMMRDCWHA VPSQRPTFKQLVEVLDRIVALTSNQ 675
          RMDKP+NCTNELYMMMRDCWHA VPSQRPTFKQLVE LDRI+ LT+N+
Sbjct: 722 RMDKPANCTNELYMMMRDCWHA VPSQRPTFKQLVEDLDRILTLTTNE 768

```

sp\_vs P21802-4 Isoform 4 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 682 AA  
FGFR2\_HUMAN (Human)] align

Score = 1029 bits (2661), Expect = 0.0  
Identities = 507/676 (75%), Positives = 570/676 (84%), Gaps = 14/676 (2%)

```

Query: 1 MWGKCLLFWAVLVATLCTARPA-----PTLPEQDALPSSDDDDDDSSSEKETDN 54
          M W + V+ ATL ARP+ TL +DA+ S +D+DD D + E N
Sbjct: 1 MVSWGRIICLVVVTMTLSLARPSFSLVEDTTLEPEDAISSGDEDDDTGAEDFVSENSN 60
Query: 55 TKPNPVAPYWTSPKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGG 114
          K APYWT+ EKMEK+LHAVPAA TVKF+CP+ G P PT+RWLKNGKEFK +HRIGG
Sbjct: 61 NKR---APYWTNTEKMEKKRLHAVPAANTVKFRCPAGGNPMTMRWLKNGKEFKQEHRRIGG 117
Query: 115 YKVRYATWSIIMDSVVP SDKGN YTCIVENEYGSINHTYQLDVVERSPhRPILQAGLPAN 174

```

```

      YKVR  WS+IM+SVVPSDKGNYTC+VENEYGSINHTY LDVVERSPHRPILQAGLPAN
Sbjct: 118 YKVRNQHWSLIMESVVPSPDKGNYTCVVENEYGSINHTYHLDVVERSPHRPILQAGLPANA 177

Query: 175 TVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPPYQILKHSGINSSDAEVL 234
      + +G +VEF+CKVYSD QPHIQW+KH+E NGSK GPD LPY+++LKHSGINSS+AEVL
Sbjct: 178 STVVGGDVEFVCKVYSDAQPHIQWIKHVEKNGSKYGPDLPLKVLKHSGINSSNAEVL 237

Query: 235 LFNVTQAQSGEYVCKVSNYIGEANQSAWLTVTRPVAKALEERPAMVMTSPLYLEIIYCTG 294
      LFNVTQA +GEY+CKVSNYIG+ANQSAWLTV P +A + SP YLEI IYC G
Sbjct: 238 LFNVTQAQSGEYVCKVSNYIGEANQSAWLTVL- PKQQAPGREKETASPDYLEIAIYCI 296

Query: 295 AFLISCMLGSVIIYKMKSGTKKSDFHSMQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLL 354
      FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K IPLRRQV SA+SS+SMNS L
Sbjct: 297 VFLLIACMVVTVILCRMKNNTTKKPDFSSQPAVHKLTKRIPLRRQV--SAESSSSMNSNTPL 354

Query: 355 VR-PSRLSSG-TPMLAGVSEYELPEDPRWELPRDLRLVLGKPLGEGCFQGVVLAEAIGLD 412
      VR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+L LGKPLGEGCFQGVV+AEA+G+D
Sbjct: 355 VRITTRLSSSTADTPMLAGVSEYELPEDPKWEFPRDKLTGKPLGEGCFQGVVMAEAVGID 414

Query: 413 KDKPNRVTKVAVKMLKSDATEKDLSLISEMEMMKMIGKHKNIINLLEACTQDGPLYVIV 472
      KDKP VAVKMLK DATEKDLSL+SEMEMMKMIGKHKNIINLL ACTQDGPLYVIV
Sbjct: 415 KDKPKEAVTVAVKMLKDATEKDLSLSEMEMMKMIGKHKNIINLLGACTQDGPLYVIV 474

Query: 473 EYASKGNLREYLQARRPPGLEIYCYNPSHNPEEQLSKDLVSCAYQVARGMEYLASKKCIH 532
      EYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++ KDLVSC YQ+ARGMEYLAS+KCIH
Sbjct: 475 EYASKGNLREYLARRPPGMEYSYDINRVPEEQMTFKDLVSCYQLARGMEYLASQKCIH 534

Query: 533 RDLAARNVLVTEEDNVMKIADFGGLARDIHHIDYKKTNGRLPVKWMAPALFDRYTHQS 592
      RDLAARNVLVTE+NVMKIADFGGLARDI++IDYKKTNGRLPVKWMAPALFDR+YTHQS
Sbjct: 535 RDLAARNVLVTEENVMKIADFGGLARDINNIDYKKTNGRLPVKWMAPALFDRVYTHQS 594

Query: 593 DVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVP 652
      DVWSFGVL+WEIFTLGGSPYPG+PVEELFKLLKEGHRMDK+P+NCTNELYMMMRDCWHAVP
Sbjct: 595 DVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKEGHRMDKPNCTNELYMMMRDCWHAVP 654

Query: 653 SQRPTFKQLVEVLDRI 668
      SQRPTFKQLVE LDRI
Sbjct: 655 SQRPTFKQLVEDLDRI 670

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```

tr Q1KHY5 Fibroblast growth factor receptor 2 (Bacteria-expressed kinase, 785 AA
Q1KHY5_HUMAN keratinocyte growth factor receptor, craniofacial
              dysostosis 1, Crouzon syndrome, Pfeiffer syndrome,
              Jackson-Weiss syndrome) [FGFR2] [Homo sapiens (Human)] align

```

Score = 1011 bits (2615), Expect = 0.0  
 Identities = 495/669 (73%), Positives = 563/669 (84%), Gaps = 13/669 (1%)

```

Query: 31 DALPSSSEDDDDSSSEKETDNTKPNPVAPYWTSPKMEKKLHAVPAAKTVKFKCPSS 90
      DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
Sbjct: 126 DAISSEDEDDTDGAEDFVSENSNNKR---APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182

Query: 91 GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSPDKGNYTCIVENEYGSINH 150
      G P PT+RWLKNGKEFK +HRIGGYKVR WS+IM+SVVPSDKGNYTC+VENEYGSINH
Sbjct: 183 GNMPTMRWLKNGKEFKQEHRIIGGYKVRNQHWSLIMESVVPSPDKGNYTCVVENEYGSINH 242

Query: 151 TYQLDVVERSPHRPILQAGLPANKTVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
      TY LDVVERSPHRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
Sbjct: 243 TYHLDVVERSPHRPILQAGLPANASTVVGGDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPPYQILKHSGINSSDAEVLTLF--NVTEAQSGEYVCKVSNYIGEANQSAWLTVTRP 268
      PD LPY+++LK +G+N++D E+ L+ NVT +GEY C N IG + SAWLTV
Sbjct: 303 PDGLPYLKLKAAAGVNTTDEIEVLYIRNVTTFEDAGEYTCLAGNSIGISPHSAWLTVLPA 362

Query: 269 VAKALEERPAMVMTSPLYLEIIYCTGAFLISCMLGSVIIYKMKSGTKKSDFHSMQMAVHKL 328
      + E + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL
Sbjct: 363 PGREKE---ITASPDYLEIAIYCIYGVFLIACMVVTVILCRMKNNTTKKPDFSSQPAVHKL 418

Query: 329 AKSIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSG-TPMLAGVSEYELPEDPRWELPR 386
      K IPLRRQV SA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PR
Sbjct: 419 TKRIPLRRQV--SAESSSSMNSNTPLVRITTRLSSSTADTPMLAGVSEYELPEDPKWEFPR 476

Query: 387 DRLVLGKPLGEGCFQGVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSLISEMEMM 446
      D+L LGKPLGEGCFQGVV+AEA+G+DKDKP VAVKMLK DATEKDLSL+SEMEMM
Sbjct: 477 DKLTGKPLGEGCFQGVVMAEAVGIDKDKPKEAVTVAVKMLKDATEKDLSLSEMEMM 536

Query: 447 KMIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLEIYCYNPSHNPEEQ 506
      KMIGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ+
Sbjct: 537 KMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLARRPPGMEYSYDINRVPEEQM 596

Query: 507 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEEDNVMKIADFGGLARDIHHIDYK 566
      + KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NVMKIADFGGLARDI++IDYK
Sbjct: 597 TFKDLVSCYQLARGMEYLASQKCIHRDLAARNVLVTEENVMKIADFGGLARDINNIDYK 656

Query: 567 KTTNGRLPVKWMAPALFDRYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKE 626

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          KTTNGRLPVKWMAPALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPG+PVEELFKLLKE
Sbjct: 657 KTTNGRLPVKWMAPALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKE 716

          GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQ 686
Query: 627 GHRMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+EYLDLS PL+
          GHRMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTNEEYLDLSQPLEP 776
Sbjct: 717 GHRMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTNEEYLDLSQPLEP 776

          YSPSPDPDR 695
Query: 687 YSP +PD R
          YSPCYDPDR 785
Sbjct: 777 YSPCYDPDR 785

```

sp\_vs P21802-6 Isoform 6 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 785 AA align  
FGFR2\_HUMAN (Human)]

Score = 1011 bits (2615), Expect = 0.0  
Identities = 495/669 (73%), Positives = 563/669 (84%), Gaps = 13/669 (1%)

```

Query: 31 DALPSSDDDDDDSSSEKETDNTKPNFVAPYWTSPKMEKKLHAVPAAKTVKFCPS 90
          DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
Sbjct: 126 DAISSGDEDDTDGAEDFVSENSNNKR---APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182

Query: 91 GTPNPTLRWLKNGKEFKPDHRIGGYKVRATWSIIIMDSVVPKGNVTCIVENEYGSINH 150
          G P PT+RWLKNKGEFK +HRIGGYKVR WS+IM+SVVPKGNVTC+VENEYGSINH
Sbjct: 183 GNPMPTRWLKNGKEFKQEHRIIGGYKVRNQHWSLIMESVVPKGNVTCVENEYGSINH 242

Query: 151 TYQLDVVERSPHRPILQAGLPANKTVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
          TY LDVVERSPHRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
Sbjct: 243 TYHLDVVERSPHRPILQAGLPANASTVVGDDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPYVQILKHSGINSSDAEVLTLF--NVTEAQSGEYVCKVSNYIGEANQSAWLTVTRP 268
          PD LPY+++LK +G+N++D E+ L+ NVT +GEY C N IG + SAWLTV
Sbjct: 303 PDGLPYLKVLAAGVNTTDKIEVLVYIRNVTFEDAGEYTCLAGNSIGISFHSAWLTVLPA 362

Query: 269 VAKALEERPAVMTSPYLEIIYCTGAPLISCMGSLVYIYKMKSGTKKSDPHSQMAVHKL 328
          + E + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL
Sbjct: 363 PGREKE---ITASPDYLEIAIYCIYGVFLIACMVVTVILCRMKNNTTKKPDFSSQPAVHKL 418

Query: 329 AKSIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSG-TPMLAGVSEYELPEDPRWELPR 386
          K IPLRRQV SA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PR
Sbjct: 419 TKRIPLRRQV--SAESSSMNSNTPLVRITTRLSTADTPMLAGVSEYELPEDPKWEFPR 476

Query: 387 DRLVLGKPLGEGCGFQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 446
          D+L LGKPLGEGCGFQVV+AEA+G+DKDKP VAVKMLK DATEKDLSDL+SEMEMM
Sbjct: 477 DKLTGKPLGEGCGFQVVMAEAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMM 536

Query: 447 KMIGKHKNIINLLGACTQDGLYVIVEYASKGNLREYLRARRPPGLECYNPSHNPEEQ 506
          KMIGKHKNIINLL ACTQDGLYVIVEYASKGNLREYLRARRPPG+EY Y+ + PEEQ+
Sbjct: 537 KMIGKHKNIINLLGACTQDGLYVIVEYASKGNLREYLRARRPPGMEYSYDINRVPEEQM 596

Query: 507 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGFLARDIHHIDYK 566
          + KDLVSC YQ+ARGMEYLA+KCIHRDLAARNVLVTE+NVMKIADFGFLARDI++IDYK
Sbjct: 597 TPKDLVSCYQLARGMEYLAQKCIHRDLAARNVLVTENNVMKIADFGFLARDIINIDYK 656

Query: 567 KTTNGRLPVKWMAPALFDRYTHQSDVWSFGVLLWEIFTLGGSPYPG+PVEELFKLLKE 626
          KTTNGRLPVKWMAPALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPG+PVEELFKLLKE
Sbjct: 657 KTTNGRLPVKWMAPALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKE 716

Query: 627 GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQ 686
          GHRMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+EYLDLS PL+
Sbjct: 717 GHRMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTNEEYLDLSQPLEP 776

          YSPSPDPDR 695
Query: 687 YSP +PD R
          YSPCYDPDR 785
Sbjct: 777 YSPCYDPDR 785

```

sp\_vs P11362-10 Isoform 7 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 573 AA align  
FGFR1\_HUMAN (Human)]

Score = 998 bits (2579), Expect = 0.0  
Identities = 496/533 (93%), Positives = 508/533 (95%), Gaps = 8/533 (1%)

```

Query: 1 MWGKCLLFWAVLVLTATLCTARPAATLPEQDALPSSDDDDDDSSSEKETDNTKPN-- 58
          MW WKCLLFWAVLVLTATLCTARP+PTLPEQDALPSSDDDDDDSSSEKETDNTKPN
Sbjct: 1 MWGKCLLFWAVLVLTATLCTARPSPTLPEQDALPSSDDDDDDSSSEKETDNTKPNRM 60

Query: 59 PVAPYWTSPKMEKKLHAVPAAKTVKFCPSGTPNPTLRWLKNGKEFKPDHRIGGYKVR 118
          PVAPYWTSPKMEKKLHAVPAAKTVKFCPSGTPNPTLRWLKNGKEFKPDHRIGGYKVR
Sbjct: 61 PVAPYWTSPKMEKKLHAVPAAKTVKFCPSGTPNPTLRWLKNGKEFKPDHRIGGYKVR 120

```

```

Query: 119 YATWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQLDVVERSPhRPILQAGLPANKTVAL 178
YATWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQLDVVERSPhRPILQAGLPANKTVAL
Sbjct: 121 YATWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQLDVVERSPhRPILQAGLPANKTVAL 180

Query: 179 GSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPHYVQILKHSGINSSDAE--VLTLF 236
GSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPHYVQILK +G+N++D E VL L
Sbjct: 181 GSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPHYVQILKTAGVNTTDKEMEVLHLR 240

Query: 237 NVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVAKALEERPAVMTSPLYLEIIYCTGAF 296
NV+ +GEY C N IG ++ SAWLTV +ALEERPAVMTSPLYLEIIYCTGAF
Sbjct: 241 NVSFEDAGEYTCLAGNSIGLSHSAWLTVL---EALERPAVMTSPLYLEIIYCTGAF 296

Query: 297 LISCMGSGVYIYKMKSGTKKSDFHSMQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVR 356
LISCM+GSVI+YKMKSGTKKSDFHSMQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVR
Sbjct: 297 LISCMVGSVIVYKMKSGTKKSDFHSMQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVR 356

Query: 357 PSRLSSSGTPLAGVSEYELPEDPRWELPRDLVLGKPLGEGCFGQVVLAEAGLDKDKP 416
PSRLSSSGTPLAGVSEYELPEDPRWELPRDLVLGKPLGEGCFGQVVLAEAGLDKDKP
Sbjct: 357 PSRLSSSGTPLAGVSEYELPEDPRWELPRDLVLGKPLGEGCFGQVVLAEAGLDKDKP 416

Query: 417 NRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNINLLEACTQDGPLYVIVEYAS 476
NRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNINLL ACTQDGPLYVIVEYAS
Sbjct: 417 NRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNINLLGACTQDGPLYVIVEYAS 476

Query: 477 KGNLREYLQARRPPGLECYNPSHNPEEQLSKDLVSCAYQVARGMEYLASKK 529
KGNLREYLQARRPPGLECYNPSHNPEEQLSKDLVSCAYQVARGMEYLASKK
Sbjct: 477 KGNLREYLQARRPPGLECYNPSHNPEEQLSKDLVSCAYQVARGMEYLASKK 529

```

sp\_vs P21802-2 Isoform 2 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 768 AA  
FGFR2\_HUMAN (Human)] align

Score = 991 bits (2561), Expect = 0.0  
Identities = 483/649 (74%), Positives = 549/649 (84%), Gaps = 11/649 (1%)

```

Query: 31 DALPSSDDDDDDSSSEKETDNTKPNPVAPYWTSPEKMEKKLHAVFAAKTVKFKCPSS 90
DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
Sbjct: 126 DAISGDDDDTDGAEDFVSENSNNKR---APYWTNTEKMEKRLHAVFAANTVKFRCPAG 182

Query: 91 GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSPDKGNYTCIVENEYGSINH 150
G P PT+RWLKNKGEFK +HRIGGYKVR WS+IM+SVVPSPDKGNYTC+VENEYGSINH
Sbjct: 183 GNPMPMTMRWLKNGKEFKQEHRIGGYKVRNQHWSLIMESVVPSPDKGNYTCVVENEYGSINH 242

Query: 151 TYQLDVVERSPhRPILQAGLPANKTVALGSGNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
TY LDVVERSPhRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
Sbjct: 243 TYHLDVVERSPhRPILQAGLPANASTVVGGDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPHYVQILKHSGINSSDAEVLTLF--NVTEAQSGEYVCKVSNYIGEANQSAWLTVTRP 268
PD LPY+++LK +G+N++D E+ L+ NVT +GEY C N IG + SAWLTV
Sbjct: 303 PDGILPYLKVLAAGVNTTDEIEVLYIRNVTEDAGEYTCLAGNSIGISFHSWLTVLPA 362

Query: 269 VAKALEERPAVMTSPLYLEIIYCTGAFLISCMGSGVYIYKMKSGTKKSDFHSMQMAVHKL 328
+ E + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL
Sbjct: 363 PGREKE---ITASPDYLEIAIYCIGVFLIACMVVTILCRMNTTKKPDFSSQPAVHKL 418

Query: 329 AKSIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPLAGVSEYELPEDPRWELPR 386
K IPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPLAGVSEYELPEDP+WE PR
Sbjct: 419 TKRIPLRRQVTVSAAESSSSMSNTPLVRIITRLSSTADTPMLAGVSEYELPEDPKWEFPR 478

Query: 387 DRLVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 446
D+L LGKPLGEGCFGQVV+AEA+G+DKDKP VAVKMLK DATEKDLSDL+SEMEMM
Sbjct: 479 DKLTLGKPLGEGCFGQVVMMAEAVGIDKDKPKEAVTVAVKMLKDATEKDLSDLVSEMEMM 538

Query: 447 KMIGKHKNINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQ 506
KMIGKHKNINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ+
Sbjct: 539 KMIGKHKNINLLGACTQDGPLYVIVEYASKGNLREYLARRPPGMEYSYDINRVPEEQM 598

Query: 507 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTE+NVMKIADFLGARDIHHIDYK 566
+ KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NVMKIADFLGARDI++IDYK
Sbjct: 599 TFKDLVSCYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFLGARDINNIDYK 658

Query: 567 KTTNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIFTLGGSPPYGPVFEELFKLLKE 626
KTTNGRLPVKWMAPALFDR+YTHQSDVWSFGVL+WEIFTLGGSPPYG+PVEELFKLLKE
Sbjct: 659 KTTNGRLPVKWMAPALFDRVYTHQSDVWSFGVLMWEIFTLGGSPPYGPVFEELFKLLKE 718

Query: 627 GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQ 675
GHRMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+
Sbjct: 719 GHRMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTNE 767

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sp\_vs P11362-11 Isoform 9 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 571 AA  
FGFR1\_HUMAN (Human)] align

Score = 989 bits (2557), Expect = 0.0  
Identities = 494/533 (92%), Positives = 506/533 (94%), Gaps = 10/533 (1%)

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Query: 1  MWGKCLLFWAVLVLTATLCTARPAPTLPEQDALPSSSEDDDDDDSSSEKETDNTKPN-- 58
      MW WKCLLFWAVLVLTATLCTARP+PTLPEQDALPSSSEDDDDDDSSSEKETDNTKPN
Sbjct: 1  MWSKCLLFWAVLVLTATLCTARPSPTLPEQDALPSSSEDDDDDDSSSEKETDNTKPNRM 60

Query: 59  PVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVR 118
      PVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVR
Sbjct: 61  PVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVR 120

Query: 119 YATWSIIMDSVVP SDKGNYTCIVENEYGSINHTYQLD VVERS PHRPILQAGLPANKTVAL 178
      YATWSIIMDSVVP SDKGNYTCIVENEYGSINHTYQLD VVERS PHRPILQAGLPANKTVAL
Sbjct: 121 YATWSIIMDSVVP SDKGNYTCIVENEYGSINHTYQLD VVERS PHRPILQAGLPANKTVAL 180

Query: 179 GSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLFPYVQILKHSGINSSDAE--VLTLF 236
      GSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLFPYVQILK +G+N++D E VL L
Sbjct: 181 GSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLFPYVQILKTAGVNTTDKEMEVLHLR 240

Query: 237 NVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVAKALEERPAMVMTSPLYLEIIIIYCTGAF 296
      NV+ +GEY C N IG ++ SAWLTV +ALEERPAMVMTSPLYLEIIIIYCTGAF
Sbjct: 241 NVSFEDAGEYTCLAGNSIGLSHSAWLTVL---EALERPAVMTSPLYLEIIIIYCTGAF 296

Query: 297 LISCMGSGSVIIYKMKSGTKKSDFHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVR 356
      LISCM+GSVI+YKMKSGTKKSDFHSQMAVHKLAKSIPLRRQV SADSSASMNSGVLLVR
Sbjct: 297 LISCMVGSVIVYKMKSGTKKSDFHSQMAVHKLAKSIPLRRQV--SADSSASMNSGVLLVR 354

Query: 357 PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEIIGLDKDKP 416
      PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEIIGLDKDKP
Sbjct: 355 PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEIIGLDKDKP 414

Query: 417 NRVTKVAVKMLKSDATEKDLSLISEMEMMKMIGKHKNIINLLEACTQDGPLYVIVEYAS 476
      NRVTKVAVKMLKSDATEKDLSLISEMEMMKMIGKHKNIINLL ACTQDGPLYVIVEYAS
Sbjct: 415 NRVTKVAVKMLKSDATEKDLSLISEMEMMKMIGKHKNIINLLGACTQDGPLYVIVEYAS 474

Query: 477 KGNLREYLQARRPPGLECYNPSHNPEEQ LSSKDLVSCAYQVARGMEYLASKK 529
      KGNLREYLQARRPPGLECYNPSHNPEEQ LSSKDLVSCAYQVARGMEYLASKK
Sbjct: 475 KGNLREYLQARRPPGLECYNPSHNPEEQ LSSKDLVSCAYQVARGMEYLASKK 527

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sp\_vs P21802-8 Isoform 8 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 766 AA  
FGFR2\_HUMAN (Human)] align

Score = 982 bits (2539), Expect = 0.0  
Identities = 481/649 (74%), Positives = 547/649 (84%), Gaps = 13/649 (2%)

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Query: 31  DALPSSSEDDDDDDSSSEKETDNTKPNPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSS 90
      DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
Sbjct: 126 DATSSGDEDDDDTGAEDFVSENSNNKR---APYWTNTEKMEKRLHAVPAANTVVFRCFAG 182

Query: 91  GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSINH 150
      G P PT+RWLKNKGEFK +HRIGGYKVR WS+IM+SVVPSDKGNYTC+VENEYGSINH
Sbjct: 183 GNPMPMTRWLKNGKEFKQEHRIIGGYKVRNQHWSLIMESVVP SDKGNYTCVENEYGSINH 242

Query: 151 TYQLD VVERS PHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
      TY LDVVERS PHRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
Sbjct: 243 TYHLD VVERS PHRPILQAGLPANASTVVG DVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLFPYVQILKHSGINSSDAEVLTLF--NVTEAQSGEYVCKVSNYIGEANQSAWLTVTRP 268
      PD LPY+++LK +G+N++D E+ L+ NVT +GEY C N IG + SAWLTV
Sbjct: 303 PDGLPYLKVLAAGVNTTDKEIEVLVIRNVT FEDAGEYTCLAGNSIGISFSAWLTVLPA 362

Query: 269 VAKALEERPAMVMTSPLYLEIIIIYCTGAFLISCMGSGSVIIYKMKSGTKKSDFHSQMAVHKL 328
      + E + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL
Sbjct: 363 PGREKE---ITASPDYLEIAIYCIGVFLIACMVVTVILCRMKNTTKKPDFSSQPAVHKL 418

Query: 329 AKSIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPR 386
      K IPLRRQV SA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PR
Sbjct: 419 TKRIPLRRQV--SAESSSSMNSNTPLVRITRLSSSTADTPMLAGVSEYELPEDPKWEFPR 476

Query: 387 DRLVLGKPLGEGCFGQVVLAEIIGLDKDKPNRVTKVAVKMLKSDATEKDLSLISEMEMM 446
      D+L LGKPLGEGCFGQV+AEA+G+DKDKP VAVKMLK DATEKDLSL+SEMEMM
Sbjct: 477 DKLTILGKPLGEGCFGQVVM AEAVGIDKDKPEAVTVAVKMLKD DATEKDLSL+SEMEMM 536

Query: 447 KMIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQ L 506
      KMIGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ+
Sbjct: 537 KMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLRRARRPPGMEYSYDINRVPEEQM 596

Query: 507 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTE DNVMKIADFLGARDIHHIDYYK 566
      + KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NVMKIADFLGARDI++IDYYK
Sbjct: 597 TFKDLVSCYQLARGMEYLASQKCIHRDLAARNVLVTE NNVMKIADFLGARDI NNIDYYK 656

Query: 567 KTTNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVPEELFKLLKE 626
      KTTNGRLPVKWMAPALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPG+PVEELFKLLKE

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Sbjct: 657 KTTNGRLPVKWMPEALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKE 716  
 Query: 627 GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTPKQLVEVLDRIVALTSNQ 675  
 GHRMDKP+NCTNELYMMMRDCWHAVPSQRPTPKQLVE LDRI+ LT+N+  
 Sbjct: 717 GHRMDKPFANCTNELYMMMRDCWHAVPSQRPTPKQLVEDLDRIILTITNE 765

sp\_vs P11362-8 Isoform 2 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 662 AA  
 FGFR1\_HUMAN (Human)] align

Score = 934 bits (2415), Expect = 0.0  
 Identities = 468/503 (93%), Positives = 479/503 (95%), Gaps = 8/503 (1%)

Query: 31 DALPSSSEDDDDDDSSSEKETDNTKPN--PVAPYWTSPEKMEKKLHAVPAAKTVKFKCP 88  
 DALPSSSEDDDDDDSSSEKETDNTKPN PVAPYWTSPEKMEKKLHAVPAAKTVKFKCP  
 Sbjct: 120 DALPSSSEDDDDDDSSSEKETDNTKPNRMPVAPYWTSPEKMEKKLHAVPAAKTVKFKCP 179  
 Query: 89 SSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSI 148  
 SSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSI  
 Sbjct: 180 SSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSI 239  
 Query: 149 NHTYQLDVVERSHPRPILQAGLPANKTVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSK 208  
 NHTYQLDVVERSHPRPILQAGLPANKTVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSK  
 Sbjct: 240 NHTYQLDVVERSHPRPILQAGLPANKTVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSK 299  
 Query: 209 IGPDLNLPYVQILKHSGINSSDAE--VLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVT 266  
 IGPDLNLPYVQILK +G+N++D E VL L NV+ +GEY C N IG ++ SAWLTV  
 Sbjct: 300 IGPDLNLPYVQILKTAGVNTTDKEMEVLHLNRVSFEDAGEYTCLAGNSIGLSHHSAWLTVL 359  
 Query: 267 RPAKALEERPAVMTSPLYLEIIIIYCTGAFLISCMVGSIIYKMKSGTKKSDFHSQMAVH 326  
 +ALEERPAVMTSPLYLEIIIIYCTGAFLISCM+GSVI+YKMKSGTKKSDFHSQMAVH  
 Sbjct: 360 ----EALERPAVMTSPLYLEIIIIYCTGAFLISCMVGSIVIVYKMKSGTKKSDFHSQMAVH 415  
 Query: 327 KLAKSIPLRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR 386  
 KLAKSIPLRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR  
 Sbjct: 416 KLAKSIPLRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR 475  
 Query: 387 DRLVLGKPLGEGCGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 446  
 DRLVLGKPLGEGCGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM  
 Sbjct: 476 DRLVLGKPLGEGCGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 535  
 Query: 447 KMIGKHKNIINLL EACTODGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQ 506  
 KMIGKHKNIINLL ACTODGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQ  
 Sbjct: 536 KMIGKHKNIINLL GACTODGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQ 595  
 Query: 507 SSKDLVSCAYQVARGMEYLASKK 529  
 SSKDLVSCAYQVARGMEYLASKK  
 Sbjct: 596 SSKDLVSCAYQVARGMEYLASKK 618

Score = 90.5 bits (223), Expect = 9e-18  
 Identities = 78/307 (25%), Positives = 118/307 (38%), Gaps = 83/307 (27%)

Query: 1 MWGWKCLLFWAVLVLTATLCTARPAPTLPEQDALPSSSEDDDDDDSSSEKETDNTKPNPV 60  
 MW WKCLLFWAVLVLTATLCTARP+PTLPEQ  
 Sbjct: 1 MWSWKCLLFWAVLVLTATLCTARPSPTLPEQ----- 30  
 Query: 61 APYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA 120  
 A W +P ++E L V ++ +C ++ WL++G + +R R  
 Sbjct: 31 AQPWGAPVEVESFL--VHPGDLQLRCLRLDDVQ--SINWLRDGVQLAESNR-----TRIT 82  
 Query: 121 TWSIIMDSVVP SDKGNYTCIVENEYGSINHTYQLDVVERS----- 161  
 + + VP+D G Y C+ + GS + ++V + P  
 Sbjct: 83 GEEVEVQDSVPADSGLYACVTSSPSGSDTTYFSVNVSDALPSSSEDDDDDDSSSEKETD 142  
 Query: 162 -----HRPILQAGLPANK-----TVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210  
 P+ K V V+P C P P ++WLK NG +  
 Sbjct: 143 NTKPNRMPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLK---NGKEFK 198  
 Query: 211 PDNLPYVQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVT---- 266  
 PD+ +++ + + + +V + G Y C V N G N + L V  
 Sbjct: 199 PDHRIGGYKVRYATWS-----IIMDSVVP SDKGNYTCIVENEYGSINHTYQLDVVERS 252  
 Query: 267 -RPVAKA 272  
 RP+ +A  
 Sbjct: 253 HRPILQA 259

sp P22607 Fibroblast growth factor receptor 3 precursor (EC 2.7.10.1) 806 AA  
 FGFR3\_HUMAN (FGFR-3) (CD333 antigen) [FGFR3] [Homo sapiens (Human)] align

Score = 931 bits (2406), Expect = 0.0  
 Identities = 462/685 (67%), Positives = 552/685 (80%), Gaps = 17/685 (2%)

Query: 34 PSSSEDDDDDDSSSEKETDNTKPNPVAPYWTSPPEKMEKKLHAPPAKTVKFKCPSSGTP 93  
 PSS DD+D +D E ++T + APYWT PE+M+KKL AVPA TV+F+CP++G P  
 Sbjct: 129 PSSGDEDEDGED-----EAEDTGVDTGAPYWTRPERMDKKLLAVPAANTVRFRCPAAGNP 182

Query: 94 NPTLRWLKNGKEFKPDHRIGGYKVRATWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQ 153  
 P++ WLKNG+EF+ +HRIGG K+R+ WS++M+SVVPSD+GNYTC+VEN++GSI TY  
 Sbjct: 183 TPSISWLKNGREFRGEHRIGGIKLRHQWLSVMESVVPDRGNYTCVENKFGSIRQTYT 242

Query: 154 LDVVERSHPRPILQAGLPANKTVALGSNVFPMCKVSDPQPHIQWLKHIEVNGSKIGPDN 213  
 LDV+ERSHPRPILQAGLPAN+T LGS+VEF CKVYSD QPHIQWLKH+EVNGSK+GPD  
 Sbjct: 243 LDVLEERSHPRPILQAGLPANQTAVLGSDVEFHCKVYSDAQPHIQWLKHIEVNGSKVGPDPG 302

Query: 214 LPYVQILKHSGINSDDAE--VLTFLNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPAK 271  
 PYV +LK +G N++D E VL+L NVT +GEY C N IG ++ SAWL V P +  
 Sbjct: 303 TPVTVLKTAGANTTDEKELEVLSLHNVTFEDAGEYTCLAGNSIGFSHHSANLVLV-PAEE 361

Query: 272 ALEERPAVMTSPLYLEIIYCTGAFLISCMGLSVIIYKMKSGTKKSDFSQMAVHKLAKS 331  
 L E A +Y I+ Y G FL ++ +V + +++S KK VHK+++  
 Sbjct: 362 ELVE--ADEAGSVYAGILSYGVGFLLFILVVAAVTLCRLRSPPKKG--LGSPTVHKISR- 416

Query: 332 IPLRRQVTVSADSSASMSNGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDRVL 391  
 PL+RQV S +S+ASM+S LVR +RLSS P LA VSE ELP DP+WEL R RL L  
 Sbjct: 417 FPLKRQV--SLESNASMSNTPLVRIARLSSGEGPTLANVSELELPADPKWELSRARLTL 474

Query: 392 GKPLGEGCFGQVVLAAEIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGK 451  
 GKPLGEGCFGQVV+AEAIG+DKD+ + VAVKMLK DAT+KDLSDL+SEMEMMKMIGK  
 Sbjct: 475 GKPLGEGCFGQVMAEAIGIDKRAAKPVTAVKMLKDDATDKDLSDLVSEMEMMKMIGK 534

Query: 452 HKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSPHNPEEQLSKDL 511  
 HKNIINLL ACTQ GPLVY+VEYA+KGNLRE+L+ARRPPGL+Y ++ PEEQL+ KDL  
 Sbjct: 535 HKNIINLLGACTQCGPLVVLVEYAAKGNLREPLRARRPPGLDYSEDTCKPPEQLTFKDL 594

Query: 512 VSCAYQVARGMEYLASKKCIHRDLAARNVLVTEEDNMKIADFGGLARDIHHIDYKKTNG 571  
 VSCAYQVARGMEYLAS+KCIHRDLAARNVLVTEEDNMKIADFGGLARD+H++DYKKTNG  
 Sbjct: 595 VSCAYQVARGMEYLASQKCIHRDLAARNVLVTEEDNMKIADFGGLARDVHNLDDYKKTNG 654

Query: 572 RLPVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVEELFKLLKEGHRMD 631  
 RLPVKWMAPEALFDR+YTHQSDVWSFGVLLWEIFTLGGSPYPGP+PVEELFKLLKEGHRMD  
 Sbjct: 655 RLPVKWMAPEALFDRVYTHQSDVWSFGVLLWEIFTLGGSPYPGPVEELFKLLKEGHRMD 714

Query: 632 KPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQYSPSF 691  
 KP+NCT++LYM+MR+CWAH PSQRPTFKQLVE LDR++ +TS EYLDLS P +QYSP  
 Sbjct: 715 KPANCTHIDLYMIMRECWAHAPSQRPTFKQLVEDLDRVLTSTDEYLDLSAPPEQYSPSG 774

Query: 692 PDTRSSSTCSSGDSVFSHEPLPEEP 716  
 DT SS+ SSG+DSVF+H+ LP P  
 Sbjct: 775 QDTPSSS-SSGDSVFAHDLPPAP 798

tr Q8NI15 Fibroblast growth factor receptor 3 (Fragment) [FGFR3] [Homo 769 AA  
 Q8NI15\_HUMAN sapiens (Human)] align

Score = 931 bits (2406), Expect = 0.0  
 Identities = 462/685 (67%), Positives = 552/685 (80%), Gaps = 17/685 (2%)

Query: 34 PSSSEDDDDDDSSSEKETDNTKPNPVAPYWTSPPEKMEKKLHAPPAKTVKFKCPSSGTP 93  
 PSS DD+D +D E ++T + APYWT PE+M+KKL AVPA TV+F+CP++G P  
 Sbjct: 92 PSSGDEDEDGED-----EAEDTGVDTGAPYWTRPERMDKKLLAVPAANTVRFRCPAAGNP 145

Query: 94 NPTLRWLKNGKEFKPDHRIGGYKVRATWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQ 153  
 P++ WLKNG+EF+ +HRIGG K+R+ WS++M+SVVPSD+GNYTC+VEN++GSI TY  
 Sbjct: 146 TPSISWLKNGREFRGEHRIGGIKLRHQWLSVMESVVPDRGNYTCVENKFGSIRQTYT 205

Query: 154 LDVVERSHPRPILQAGLPANKTVALGSNVFPMCKVSDPQPHIQWLKHIEVNGSKIGPDN 213  
 LDV+ERSHPRPILQAGLPAN+T LGS+VEF CKVYSD QPHIQWLKH+EVNGSK+GPD  
 Sbjct: 206 LDVLEERSHPRPILQAGLPANQTAVLGSDVEFHCKVYSDAQPHIQWLKHIEVNGSKVGPDPG 265

Query: 214 LPYVQILKHSGINSDDAE--VLTFLNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPAK 271  
 PYV +LK +G N++D E VL+L NVT +GEY C N IG ++ SAWL V P +  
 Sbjct: 266 TPVTVLKTAGANTTDEKELEVLSLHNVTFEDAGEYTCLAGNSIGFSHHSANLVLV-PAEE 324

Query: 272 ALEERPAVMTSPLYLEIIYCTGAFLISCMGLSVIIYKMKSGTKKSDFSQMAVHKLAKS 331  
 L E A +Y I+ Y G FL ++ +V + +++S KK VHK+++  
 Sbjct: 325 ELVE--ADEAGSVYAGILSYGVGFLLFILVVAAVTLCRLRSPPKKG--LGSPTVHKISR- 379

Query: 332 IPLRRQVTVSADSSASMSNGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDRVL 391  
 PL+RQV S +S+ASM+S LVR +RLSS P LA VSE ELP DP+WEL R RL L  
 Sbjct: 380 FPLKRQV--SLESNASMSNTPLVRIARLSSGEGPTLANVSELELPADPKWELSRARLTL 437

Query: 392 GKPLGEGCFGQVVLAAEIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGK 451  
 GKPLGEGCFGQVV+AEAIG+DKD+ + VAVKMLK DAT+KDLSDL+SEMEMMKMIGK



Sbjct: 438 GKPLGEGCFGQVVMMAEAGIDKDRRAKPVTVAVKMLKDDATDKDLSDLVSEMEMMMKIGK 497

Query: 452 HKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQLSSKDL 511  
 HKNIINLL ACTQ GPLYV+VEYA+KGNLRE+L+ARRPPGL+Y ++ PEEQL+ KDL

Sbjct: 498 HKNIINLLGACTQGGPLYVLVEYAAKGNLREFLRARRPPGLDYSFDTCKPPEEQLTFKDL 557

Query: 512 VSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNMKIDFGLARDIHHIDYKKTNG 571  
 VSCAYQVARGMEYLAS+KCIHRDLAARNVLVTEDNMKIDFGLARD+H++DYKKTNG

Sbjct: 558 VSCAYQVARGMEYLASQKCIHRDLAARNVLVTEDNMKIDFGLARDVHNLDYKKTNG 617

Query: 572 RLPVKWMAPEALFDRITYTHQSDVWSFGVLLWEIFTLGGSPYPGVPVEELFKLLKEGHRMD 631  
 RLPVKWMAPEALFDR+YTHQSDVWSFGVLLWEIFTLGGSPYPG+PVEELFKLLKEGHRMD

Sbjct: 618 RLPVKWMAPEALFDRVYTHQSDVWSFGVLLWEIFTLGGSPYPGIPVEELFKLLKEGHRMD 677

Query: 632 KPSNCTNELYMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQYSPSPF 691  
 KP+NCT++LYM+MR+CWAH PSQRPTFKQLVE LDR++ +TS EYLDLS P +QYSP

Sbjct: 678 KPANCHDLYMIMRECWAHAPSQRPTFKQLVEDLDRVLTVTSTDEYLDLSAPFEQYSPGG 737

Query: 692 PDTRSSCTSSGSDSVFSHEPLPEEP 716  
 DT SS+ SSG+DSVF+H+ LP P

Sbjct: 738 QDTPSSS-SSGDDSVFAHDLPPAP 761

tr Q8NI16 Fibroblast growth factor receptor 3 (Fragment) [FGFR3] [Homo 771 AA  
 Q8NI16\_HUMAN sapiens (Human)] align

Score = 929 bits (2402), Expect = 0.0  
 Identities = 459/684 (67%), Positives = 551/684 (80%), Gaps = 13/684 (1%)

Query: 34 PSSDDDDDDSSSEKETDNTKPNPVAPYWTSPKMEKKLHVPAAKTVKFKCPSSGTP 93  
 PSS DD+D +D E ++T + APYWT PE+M+KKL AVPA TV+F+CP++G P

Sbjct: 92 PSSGDDDEDGED-----EADTGVDTGAPYWTRPERMDKKLLAVPAANTVRFRCPAAGNP 145

Query: 94 NPTLRWLKNGKEFKPDHRIGGYKRYATWSIIMDSVVP SDKGNYTCIVENEYGSINHTYQ 153  
 P++ WLKNG+EF+ +HRIGG K+R+ WS++M+SVVPSD+GNYTC+VEN++GSI TY

Sbjct: 146 TPSISWLKNGREFRGEHRIGGIKLRHQQWSLVMSVVP SDRGNYTCVVENKFGSIRQTYT 205

Query: 154 LDVVERSPHRPILQAGLPANKTVALGSSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDN 213  
 LDV+ERSPHRPILQAGLPAN+T LGS+VEF CKVYSD QPHIQWLKH+EVNGSK+GPD

Sbjct: 206 LDVLESPHRPILQAGLPANQTAVLGSDVEFHCKVYSDAQPHIQWLKHIEVNGSKVGPDPG 265

Query: 214 LPYVQILKHSGINSDDAEV-LTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVAKA 272  
 PYV +LK S +A+V L L NV+E GEY+C+ +N+IG A ++ WL+V P A

Sbjct: 266 TPYVTVLKSWISEVADVRLRLANVSERDGGEYLCRATNFIGVAEKAFWLSVHGPRAAE 325

Query: 273 LEERPAVMTSPLYLEIIIIYCTGAPLISCMLGSVIIYKMKSGTKKSDFHSMQMAVHKLAKSI 332  
 E A +Y I+ Y G FL ++ +V + +++S KK VHK+++

Sbjct: 326 EELVEADEAGSSVYAGILSYGVGFLLFILVVAATLCLRLSPPKKG--LGSPTVHKISR-F 382

Query: 333 PLRRQVTVSADSSASMNSGVLVLRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDLVLG 392  
 PL+RQV S +S+ASM+S LVR +RLSS P LA VSE ELP DP+WEL R RL LG

Sbjct: 383 PLKRQV--SLESNASMSSNTPLVRIARLSSGEGPTLANVSELELPADPKWELSRARLTG 440

Query: 393 KPLGEGCFGQVVLAAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMMKIGKH 452  
 KPLGEGCFGQVV+AEAIG+DKD+ + VAVKMLK DAT+KDLSDL+SEMEMMMKIGKH

Sbjct: 441 KPLGEGCFGQVVMMAEAGIDKDRRAKPVTVAVKMLKDDATDKDLSDLVSEMEMMMKIGKH 500

Query: 453 KNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQLSSKDLV 512  
 KNIINLL ACTQ GPLYV+VEYA+KGNLRE+L+ARRPPGL+Y ++ PEEQL+ KDLV

Sbjct: 501 KNIINLLGACTQGGPLYVLVEYAAKGNLREFLRARRPPGLDYSFDTCKPPEEQLTFKDLV 560

Query: 513 SCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNMKIDFGLARDIHHIDYKKTNGR 572  
 SCAYQVARGMEYLAS+KCIHRDLAARNVLVTEDNMKIDFGLARD+H++DYKKTNGR

Sbjct: 561 SCAYQVARGMEYLASQKCIHRDLAARNVLVTEDNMKIDFGLARDVHNLDYKKTNGR 620

Query: 573 LPVKWMAPEALFDRITYTHQSDVWSFGVLLWEIFTLGGSPYPGVPVEELFKLLKEGHRMDK 632  
 LPVKWMAPEALFDR+YTHQSDVWSFGVLLWEIFTLGGSPYPG+PVEELFKLLKEGHRMDK

Sbjct: 621 LPVKWMAPEALFDRVYTHQSDVWSFGVLLWEIFTLGGSPYPGIPVEELFKLLKEGHRMDK 680

Query: 633 PSNCTNELYMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQYSPSPF 692  
 P+NCT++LYM+MR+CWAH PSQRPTFKQLVE LDR++ +TS EYLDLS P +QYSP

Sbjct: 681 PANCHDLYMIMRECWAHAPSQRPTFKQLVEDLDRVLTVTSTDEYLDLSAPFEQYSPGG 740

Query: 693 DTRSSCTSSGSDSVFSHEPLPEEP 716  
 DT SS+ SSG+DSVF+H+ LP P

Sbjct: 741 DTPSSS-SSGDDSVFAHDLPPAP 763

sp\_vs F22607-2 Isoform 2 of P22607 - Homo sapiens (Human) [FGFR3] [Homo sapiens 808 AA  
 FGFR3\_HUMAN (Human)] align

Score = 929 bits (2402), Expect = 0.0  
 Identities = 459/684 (67%), Positives = 551/684 (80%), Gaps = 13/684 (1%)

Query: 34 PSSSEDDDDDDSSSEKETDNTKPNPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTP 93  
 PSS DD+D +D E ++T + APYWT PE+M+KKL AVPA TV+F+CP++G P  
 Sbjct: 129 PSSGDDDEDGED-----EAEDTGVDTGAPYWTRPERMDKKLLAVPAANTVRFRCPAAGNP 182

Query: 94 NPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQ 153  
 P++ WLKNG+EF+ +HRIGG K+R+ WS++M+SVVPSD+GNYTC+VEN++GSI TY  
 Sbjct: 183 TPGISWLKNGREFRGEHRIGGIKLRHQQWSLVMSVVPSPDRGNYTCVENKFGSIRQTYT 242

Query: 154 LDVVERSPhRPILQAGLPANKTVALGSNVEFMCKVSDPQPHIQWLKHIEVNGSKIGPDN 213  
 LDV+ERSPhRPILQAGLPAN+T LGS+VEF CKVYSD QPHIQWLKH+EVNGSK+GPD  
 Sbjct: 243 LDVLERSPhRPILQAGLPANQTAVLGSDFEFHCKVYSDAQPHIQWLKHIEVNGSKVGPDPG 302

Query: 214 LPYVQILKHSNGINSSDAEV-LTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVPVAKA 272  
 PYV +LK S +A+V L L NV+E GEY+C+ +N+IG A ++ WL+V P A  
 Sbjct: 303 TPYVTVLKSWISESVEADVRLRLANVSRDGGEYLCRATNFIGVAEAFWLSVHGPRAAE 362

Query: 273 LEERPAVMTSPLYLEIIYCTGAFLISCMGSLVVIYKMKSGTKKSDFHSQMAVHKLAKSI 332  
 E A +Y I+ Y G FL ++ +V + ++S KK VHK+++  
 Sbjct: 363 EELVEADEAGSVYAGILSYGVGFLLFILVVAAVTLCRLRSPPKKG--LGSPTVHKISR-F 419

Query: 333 PLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLG 392  
 PL+RQV S +S+ASM+S LVR +RLSS P LA VSE ELP DP+WEL R RL LG  
 Sbjct: 420 PLKRQV--SLESNASMSSNTPLVRIARLSSGEGPTLANVSELELPADPKWELSPARLTLG 477

Query: 393 KPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKH 452  
 KPLGEGCFGQVV+AEAIG+DKD+ + VAVKMLK DAT+KDLSDL+SEMEMMKMIGKH  
 Sbjct: 478 KPLGEGCFGQVVMABEAGIDKDRRAKPVTVAVKMLKDDATDKDLSDLVSEMEMMKMIGKH 537

Query: 453 KNIINLLEACTQDGLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQLSKDLV 512  
 KNIINLL ACTQ GPLYV+VEYA+KGNLRE+L+ARRPPGL+Y ++ PEEQL+ KDLV  
 Sbjct: 538 KNIINLLGACTQGGPLVYLVEYAAKGNLREPLRARPPGLDYSFDTCKPPPEQLTFKDLV 597

Query: 513 SCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGGLARDIHIDYVKKTTNGR 572  
 SCAYQVARGMEYLA+KCIHRDLAARNVLVTEDNVMKIADFGGLARD+H++DYVKKTTNGR  
 Sbjct: 598 SCAYQVARGMEYLAQKCIHRDLAARNVLVTEDNVMKIADFGGLARDVHNLDYVKKTTNGR 657

Query: 573 LPVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVEELFKLLKEGHRMDK 632  
 LPVKWMAPEALFDR+YTHQSDVWSFGVLLWEIFTLGGSPYPGP+PVERLFKLLKEGHRMDK  
 Sbjct: 658 LPVKWMAPEALFDRVYTHQSDVWSFGVLLWEIFTLGGSPYPGP+PVEELFKLLKEGHRMDK 717

Query: 633 PSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTNSQEYLDLSIPLDQYSPSP 692  
 P+NCT++LYM+MR+CWHA PSQRPTFKQLVE LDR++ +TS EYLDLS P +QYSP  
 Sbjct: 718 PANCTHDLYMIMRECWAAPSQRPTFKQLVEDLDRVLTSTDEYLDLSAPPEQYSPGGQ 777

Query: 693 DTRSTCSCSGEDSVFSHEFLPEEP 716  
 DT SS+ SSG+DSVF+H+ LP P  
 Sbjct: 778 DTPSSS--SSGDSVFAHDLPPAP 800

sp\_vs P11362-9 Isoform 5 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 660 AA  
 FGFR1\_HUMAN (Human)] align

Score = 926 bits (2393), Expect = 0.0  
 Identities = 466/503 (92%), Positives = 477/503 (94%), Gaps = 10/503 (1%)

Query: 31 DALPSSSEDDDDDDSSSEKETDNTKPN--PVAPYWTSPEKMEKKLHAVPAAKTVKFKCP 88  
 DALPSSSEDDDDDDSSSEKETDNTKPN PVAPYWTSPEKMEKKLHAVPAAKTVKFKCP  
 Sbjct: 120 DALPSSSEDDDDDDSSSEKETDNTKPNRMPVAPYWTSPEKMEKKLHAVPAAKTVKFKCP 179

Query: 89 SSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSPDKGNYTCIVENEYGSI 148  
 SSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSPDKGNYTCIVENEYGSI  
 Sbjct: 180 SSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSPDKGNYTCIVENEYGSI 239

Query: 149 NHTYQLDVVERSPhRPILQAGLPANKTVALGSNVEFMCKVSDPQPHIQWLKHIEVNGSK 208  
 NHTYQLDVVERSPhRPILQAGLPANKTVALGSNVEFMCKVSDPQPHIQWLKHIEVNGSK  
 Sbjct: 240 NHTYQLDVVERSPhRPILQAGLPANKTVALGSNVEFMCKVSDPQPHIQWLKHIEVNGSK 299

Query: 209 IGPDLNLPYVQILKHSNGINSSDAE--VLTFLNVTEAQSGEYVCKVSNYIGEANQSAWLTVT 266  
 IGPDLNLPYVQILK +G+N++D E VL L NV+ +GEY C N IG ++ SAWLTV  
 Sbjct: 300 IGPDLNLPYVQILKTAGVNTTDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVL 359

Query: 267 RPAKALEERPAVMTSPLYLEIIYCTGAFLISCMGSLVVIYKMKSGTKKSDFHSQMAVH 326  
 +ALEERPAVMTSPLYLEIIYCTGAFLISCM+GSVI+YKMKSGTKKSDFHSQMAVH  
 Sbjct: 360 ----EALERPAVMTSPLYLEIIYCTGAFLISCMVGSVVIYKMKSGTKKSDFHSQMAVH 415

Query: 327 KLAksiPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR 386  
 KLAksiPLRRQV SADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR  
 Sbjct: 416 KLAksiPLRRQV--SADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR 473

Query: 387 DRLVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 446  
 DRLVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM

Sbjct: 474 DRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 533  
 Query: 447 KMIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQ 506  
 KMIGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQ  
 Sbjct: 534 KMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQ 593  
 Query: 507 SSKDLVSCAYQVARGMEYLASKK 529  
 SSKDLVSCAYQVARGMEYLASKK  
 Sbjct: 594 SSKDLVSCAYQVARGMEYLASKK 616

Score = 90.5 bits (223), Expect = 9e-18  
 Identities = 78/307 (25%), Positives = 118/307 (38%), Gaps = 83/307 (27%)

Query: 1 MWGWKCLLFWAVLVTATLCTARPAPTLPEQDALPSEDDDDDDSSSEKETDNTKPNPV 60  
 MW WKCLLFWAVLVTATLCTARP+PTLPEQ  
 Sbjct: 1 MWSWKCLLFWAVLVTATLCTARPSPTLPEQ----- 30  
 Query: 61 APYWTSPKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA 120  
 A W +P ++E L V ++ +C ++ WL++G + +R R  
 Sbjct: 31 AQPWGAPEVESPL--VHPGDLQLRCRLRDDVQ-SINWLRDGVQLAESNR-----TRIT 82  
 Query: 121 TWSIIMDSVVP SDKGNYTCIVENEYGSINHTYQLDVVERSP----- 161  
 + + VP+D G Y C+ + GS + ++V + P  
 Sbjct: 83 GEEVEVQDSVPADSGLYACVTSSPSGSDTTYFSVNVSDALPSEDDDDDDSSSEKETD 142  
 Query: 162 -----HRPILQAGLPANK-----TVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210  
 P+ K V V+F C P P ++WLK NG +  
 Sbjct: 143 NTKPNRMPVAPYWTSPKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLK---NGKEFK 198  
 Query: 211 PDNLPVYQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVT--- 266  
 PD+ +++ + + + +V + G Y C V N G N + L V  
 Sbjct: 199 PDHRIGGYKVRYATWS-----IIMDSVVP SDKGNYTCIVENEYGSINHTYQLDVVERSP 252  
 Query: 267 -RPVAKA 272  
 RP+ +A  
 Sbjct: 253 HRPILQA 259

sp\_vs P11362-12 Isoform 11 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 502 AA  
 FGFR1\_HUMAN (Human)] align

Score = 857 bits (2214), Expect = 0.0  
 Identities = 429/462 (92%), Positives = 440/462 (95%), Gaps = 6/462 (1%)

Query: 70 MEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSV 129  
 MEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSV  
 Sbjct: 1 MEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSV 60  
 Query: 130 VPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGNSNVEFMCKVY 189  
 VPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGNSNVEFMCKVY  
 Sbjct: 61 VPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGNSNVEFMCKVY 120  
 Query: 190 SDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKHSGINSSDAE--VLTLFNVTEAQSGEYV 247  
 SDPQPHIQWLKHIEVNGSKIGPDNLPYVQILK +G+N++D E VL L NV+ +GEY  
 Sbjct: 121 SDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNTTKEMEVLHLRNVSFEDAGEYT 180  
 Query: 248 CKVSNYIGEANQSAWLTVTRPVAKALEERPAMVMTSPLYLEIIYCTGAPLISCMGSGVII 307  
 C N IG ++ SAWLTV +ALEERPAMVMTSPLYLEIIYCTGAPLISCM+GSGVI+  
 Sbjct: 181 CLAGNSIGLSHSAWLTVL---EALERPAMVMTSPLYLEIIYCTGAPLISCMVGSVIV 236  
 Query: 308 YKMKSGTKKSDPHSQMAVHKLAKSIPLRRQVTVSADSSASMN SGVLLVRPSRLSSSGTPM 367  
 YKMKSGTKKSDPHSQMAVHKLAKSIPLRRQVTVSADSSASMN SGVLLVRPSRLSSSGTPM  
 Sbjct: 237 YKMKSGTKKSDPHSQMAVHKLAKSIPLRRQVTVSADSSASMN SGVLLVRPSRLSSSGTPM 296  
 Query: 368 LAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKML 427  
 LAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKML  
 Sbjct: 297 LAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKML 356  
 Query: 428 KSDATEKDLSDLISEMEMMKMIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQAR 487  
 KSDATEKDLSDLISEMEMMKMIGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYLQAR  
 Sbjct: 357 KSDATEKDLSDLISEMEMMKMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLQAR 416  
 Query: 488 RPPGLECYNPSHNPEEQ LSSKDLVSCAYQVARGMEYLASKK 529  
 RPPGLECYNPSHNPEEQ LSSKDLVSCAYQVARGMEYLASKK  
 Sbjct: 417 RPPGLECYNPSHNPEEQ LSSKDLVSCAYQVARGMEYLASKK 458

sp\_vs P11362-13 Isoform 13 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 500 AA  
 FGFR1\_HUMAN (Human)] align

Score = 848 bits (2192), Expect = 0.0  
 Identities = 427/462 (92%), Positives = 438/462 (94%), Gaps = 8/462 (1%)

Query: 70 MEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSV 129  
 MEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSV  
 Sbjct: 1 MEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSV 60

Query: 130 VPSDKGNYTCIVENEYGSINHTYQLDVVERSHPRPILQAGLPANKTVALGSNVEFMCKVY 189  
 VPSDKGNYTCIVENEYGSINHTYQLDVVERSHPRPILQAGLPANKTVALGSNVEFMCKVY  
 Sbjct: 61 VPSDKGNYTCIVENEYGSINHTYQLDVVERSHPRPILQAGLPANKTVALGSNVEFMCKVY 120

Query: 190 SDPQPHIQWLKHIEVNGSKIGPDNLPHYVQILKHSGINSSDAE--VLTLFNVTEAQSGEYV 247  
 SDPQPHIQWLKHIEVNGSKIGPDNLPHYVQILK +G+N++D E VL L NV+ +GEY  
 Sbjct: 121 SDPQPHIQWLKHIEVNGSKIGPDNLPHYVQILKTAGVNTTDKEMEVLHLRNVSPEDAGEYT 180

Query: 248 CKVSNYIGEANQSAWLTVPVAKALEERPAMVMTSPLYLEIIIIYCTGAFLISCMGSGVII 307  
 C N IG ++ SAWLTV +ALEERPAMVMTSPLYLEIIIIYCTGAFLISCM+GSGVI+  
 Sbjct: 181 CLAGNSIGLSHSAWLTVL---EALERPAMVMTSPLYLEIIIIYCTGAFLISCMVGSVIV 236

Query: 308 YMKKSGTKKSDFHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTGM 367  
 YMKKSGTKKSDFHSQMAVHKLAKSIPLRRQV SADSSASMNSGVLLVRPSRLSSSGTGM  
 Sbjct: 237 YMKKSGTKKSDFHSQMAVHKLAKSIPLRRQV--SADSSASMNSGVLLVRPSRLSSSGTGM 294

Query: 368 LAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKML 427  
 LAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKML  
 Sbjct: 295 LAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKML 354

Query: 428 KSDATEKDLSDLISEMEMMKMIGKHKNIIINLLEACTQDGPLYVIVEYASKGNLREYLQAR 487  
 KSDATEKDLSDLISEMEMMKMIGKHKNIIINLL ACTQDGPLYVIVEYASKGNLREYLQAR  
 Sbjct: 355 KSDATEKDLSDLISEMEMMKMIGKHKNIIINLLGACTQDGPLYVIVEYASKGNLREYLQAR 414

Query: 488 RPPGLECYNPNSHNPEEQLSKDLVSCAYQVARGMEYLASKK 529  
 RPPGLECYNPNSHNPEEQLSKDLVSCAYQVARGMEYLASKK  
 Sbjct: 415 RPPGLECYNPNSHNPEEQLSKDLVSCAYQVARGMEYLASKK 456

sp P22455 Fibroblast growth factor receptor 4 precursor (EC 2.7.10.1) 802 AA  
 FGFR4\_HUMAN (FGFR-4) (CD334 antigen) [FGFR4] [Homo sapiens (Human)] align

Score = 839 bits (2168), Expect = 0.0  
 Identities = 432/707 (61%), Positives = 527/707 (74%), Gaps = 29/707 (4%)

Query: 18 LCTARPAP-----TLPEQDALPSSSEDDDDSSSEEKETDNTKPNPVAPYWTSPPEKME 71  
 LC AR + TL D+L SS +DD+D S + ++ P APYWT P++ME  
 Sbjct: 100 LCLARGSMIVLQNLTLITGDSLTSS--NDEDEPKSHRDPNSNRHSYPQQ-APYWTHPQRM 156

Query: 72 KKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP 131  
 KKLHAVPA TVKF+CP++G P PT+RWLK+G+ F ++RIGG ++R+ WS++M+SVVP  
 Sbjct: 157 KKLHAVPAGNTVVKRCPAAGNPTPTIRWLKDGQAAPHGENRIGGIRLRHQHWSLVMSVVP 216

Query: 132 SDKGNITCIVENEYGSINHTYQLDVVERSHPRPILQAGLPANKTVALGSNVEFMCKVYSD 191  
 SD+G YTC+VEN GSI + Y LDV+ERSHPRPILQAGLPAN T +GS+VE +CKVYSD  
 Sbjct: 217 SDRGTYTCLVENAVGSIRYNYLLDVLEERSHPRPILQAGLPANTTAVVGSDELCKVYSD 276

Query: 192 PQPHIQWLKHIEVNGSKIGPDNLPHYVQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVS 251  
 QPHIQWLKHI +NGS G D PYVQ+LK + INSS+ EVL L NV+ +GEY C  
 Sbjct: 277 AQPHIQWLKHIVINGSSFGADGFPYVQVLKTADINSSEVEVLRLNVSADAGEYTCLAG 336

Query: 252 NYIGEANQSAWLTVPVAKALEERP---AVMTSPLYLEIIIIYCTGAFLISCMGSGVIIY 308  
 N IG + QSAWLTV EE P A Y +II+Y +G+ ++ +L +Y  
 Sbjct: 337 NSIGLSYQSAWLTVLP-----BEDPTWTAAPEARYTDIILYASGSLALAVLLLLAGLY 390

Query: 309 KMKSGTKKSDFHSQ--MAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTGM 366  
 + G H + V KL++ PL RQ ++ + SS +S LVR RLSSSG  
 Sbjct: 391 R---GQALHGRHPRPPATVQKLSR-FPLARQFSLESGSSGKSSSS--LVRGVRLSSSGCPA 444

Query: 367 MLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKM 426  
 +LAG+ +LP DP WE PRDRLVLCKPLGEGCFGQVV AEA G+D +P++ + VAVKM  
 Sbjct: 445 LLAGLVSLDLPDLPWEFPRDRLVLGKPLGEGCFGQVVRAEAFGMDFARPDAQSTVAVKM 504

Query: 427 LKSDATEKDLSDLISEMEMMKMIGKHKNIIINLLEACTQDGPLYVIVEYASKGNLREYLQA 486  
 LK +A++KDL+DL+SEME+MK+IG+HKNIINLL CTQ+GPLYVIVE A+KGNLRE+L+A  
 Sbjct: 505 LKDNASDKDLADLVSEMEVMKLGIRHKNIINLLGVCTQEGPLYVIVECAAKGNLREFLRA 564

Query: 487 RPPGLECYNPNSHNPEEQLSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDN 546  
 RRPPG + + + E LS LVSCAYQVARGM+YL S+KCIHRDLAARNVLVTEDN  
 Sbjct: 565 RRPPGPDLSPDGPRSSGFLSPFVLVSCAYQVARGMQYLESRCKIHRDLAARNVLVTEDN 624

Query: 547 VMKIADPGLARDIHHIDYKKTNGRLPVKWMPEALFDRIYTHQSDVWSFGVLLWEIFT 606  
 VMKIADPGLAR +HHIDYKKT+NGRLPVKWMPEALFDR+YTHQSDVWSFG+LLWEIFT  
 Sbjct: 625 VMKIADPGLARGVHHIDYKKTNGRLPVKWMPEALFDRVYTHQSDVWSFGILLWEIFT 684

Query: 607 LGGSFPYGPVPVEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLD 666  
 LGGSFPYGP+PVEELF LL+EGHRMD+P +C ELY +MR+CWA PSQRPTFKQLVE LD

Sbjct: 685 LGGSPYPGIPVEELFSLREGHRMDRPPHCPPELYGLMRECWHAAPSQRPTFKQLVEALD 744  
 Query: 667 RIVALTSNQEYLDLSIPLDQYSPSPDTRSSSTCSSGSDSVFSHEPLP 713  
 +++ L ++EYLDL + YSPS D SSTCSS DSVFSH+PLP  
 Sbjct: 745 KVL-LAVSEEYLDLRLTFGPYSPSGDA-SSTCSS-SDSVFSHDPLP 788

tr Q8TDA0 Fibroblast growth factor receptor 4 (Fibroblast growth factor 802 AA  
 Q8TDA0\_HUMAN receptor 4, isoform CRA\_b) [FGFR4] [Homo sapiens align  
 (Human)]

Score = 839 bits (2167), Expect = 0.0  
 Identities = 432/707 (61%), Positives = 527/707 (74%), Gaps = 29/707 (4%)

Query: 18 LCTARPAP-----TLPEQDALPSSDDDDDDSSSEKETDNTKPNPVAPYWTSPPEKME 71  
 LC AR + TL D+L SS +DD+D S + ++ P APYWT P++ME  
 Sbjct: 100 LCLARGSMIVLQNLTLITGDSLTSS--NDEDEPKSHRDLNHRHSYPQQ-APYWTHPQRM 156

Query: 72 KKLHAVPAAKTVKFCPSSTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP 131  
 KKLHAVPA TVKF+CP++G P PT+RWLK+G+ F ++RIGG ++R+ WS++M+SVVP  
 Sbjct: 157 KKLHAVPAGNTVKFRCPAAGNPTPTIRWLKDGQAFHGENRIGGIRLRHQHNSLVMSVVP 216

Query: 132 SDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGNSNVEFMCKVYSD 191  
 SD+G YTC+VEN GSI + Y LDV+ERSPHRPILQAGLPAN T +GS+VE +CKVYSD  
 Sbjct: 217 SDRGTYTCLVENAVGSIRYNLYLDVLESPHRPILQAGLPANTTAVVGSVDVLLCKVYSD 276

Query: 192 QPHIQWLKHIEVNGSKIGPDNLFPYVQILKHSGINSDDAEVLTFLNVTEAQSGEYVCKVS 251  
 QPHIQWLKHI +NGS G D PYVQ+LK + INSS+ EVL L NV+ +GEY C  
 Sbjct: 277 AQPHIQWLKHIVINGSSFGADGFPYVQVLKTADINSSEVEVLYLRNVSAEDAGEYTCLAG 336

Query: 252 NYIGEANQSAWLTVTRPVAKALEERP--AVMTSPLEYLEIIYCTGAFLISCMGSGVIIY 308  
 N IG + QSAWLTV EE P A Y +II+Y +G+ ++ +L +Y  
 Sbjct: 337 NSIGLSYQSAWLTVLP-----EEDPTWTAAPPEARYTDIILYASGSLALAVLLLAGLY 390

Query: 309 KMKSGTKKSDPHSQ--MAVHKLAKSIPLRRQVTVSADSSASMSGVLLVRPSRLSSSGTP 366  
 + G H + V KL++ PL RQ ++ + SS +S LVR RLSSSG  
 Sbjct: 391 R---GQALHGRHRPPATVQKLSR-FPLARQFSLESGSSGKSSSS--LVRGVRLSSSGPA 444

Query: 367 MLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKM 426  
 +LAG+ +LP DP WE PRDRLVLGKPLGEGCFGQVV AEA G+D +P++ + VAVKM  
 Sbjct: 445 LLAGLVSLDLPLDPLWEFPDRDLVLGKPLGEGCFGQVVRAEAFGMDPARPDQASTVAVKM 504

Query: 427 LKSDATEKDLSDLISEMEMMKMIGKHNIINLLEACTQDGPLYVIVEYASKGNLREYLQA 486  
 LK +A++KDL+DL+SEME+MK+IG+HKNIINLL CTQ+GPLYVIVE A+KGNLRE+L+A  
 Sbjct: 505 LKDNASDKDLADLVSEMEVMKLGIRKHNIINLLGVCTQEGPLYVIVECAAKGNLREFLRA 564

Query: 487 RRPPGLECYCYNHSHNPQSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDN 546  
 RPPG + + + E LS LVSCAYQVARGM+YL S+KCIHRDLAARNVLVTEDN  
 Sbjct: 565 RRPPGPDLSPDGPRSSGGLSFPVLVSCAYQVARGMQYLESRKCIHRDLAARNVLVTEDN 624

Query: 547 VMKIADFLGARDIHHIDYKKTNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIFT 606  
 VMKIADFLGAR +HHIDYKKT+NGRLPVKWMAPALFDR+YTHQSDVWSFG+LLWEIFT  
 Sbjct: 625 VMKIADFLGARGVHHIDYKKTNGRLPVKWMAPALFDRVYTHQSDVWSFGILLWEIFT 684

Query: 607 LGGSPYPGPVPEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAAPSQRPTFKQLVEVLD 666  
 LGGSPYPG+PVEELF LL+EGHRMD+P +C ELY +MR+CWHA PSQRPTFKQLVE LD  
 Sbjct: 685 LGGSPYPGIPVEELFSLREGHRMDRPPHCPPELYGLMRECWHAAPSQRPTFKQLVEALD 744

Query: 667 RIVALTSNQEYLDLSIPLDQYSPSPDTRSSSTCSSGSDSVFSHEPLP 713  
 +++ L ++EYLDL + YSPS D SSTCSS DSVFSH+PLP  
 Sbjct: 745 KVL-LAVSEEYLDLRLTFGPYSPSGDA-SSTCSS-SDSVFSHDPLP 788

tr Q71TW8 Fibroblast growth factor receptor 4, soluble-form splice variant 762 AA  
 Q71TW8\_HUMAN [FGFR4] [Homo sapiens (Human)] align

Score = 805 bits (2078), Expect = 0.0  
 Identities = 414/700 (59%), Positives = 501/700 (71%), Gaps = 55/700 (7%)

Query: 18 LCTARPAPTLPEQDAL---PSSDDDDDDSSSEKETDNTKPNPVAPYWTSPPEKMEKK 73  
 LC AR + + + L S+ +DD+D S + ++ P APYWT P++MEKK  
 Sbjct: 100 LCLARGSMIVLQNLTLITGDSSTSSNDEDEPKSHRDLNHRHSYPQQ-APYWTHPQRM 158

Query: 74 LHAVPAAKTVKFCPSSTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP 133  
 LHAVPA TVKF+CP++G P PT+RWLK+G+ F +RIGG ++R+ WS++M+SVVPSD  
 Sbjct: 159 LHAVPAGNTVKFRCPAAGNPTPTIRWLKDGQAFHGGNRIGGIRLRHQHNSLVMSVVP 218

Query: 134 KGNVTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGNSNVEFMCKVYSDPQ 193  
 +G YTC+VEN GSI + Y LDV+ERSPHRPILQAGLPAN T +GS+VE +CKVYSD Q  
 Sbjct: 219 RGTYTCLVENAVGSIRYNLYLDVLESPHRPILQAGLPANTTAVVGSVDVLLCKVYSDAQ 278

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Query: 194 PHIQWLKHIEVNGSKIGPDNLPYVQILKHSNGINSSDAEVLTLFNVTEAQSGEYVCKVSNY 253
PHIQWLKHI +NGS G D PYVQ+LK + INSS+ EVL L NV+ +GEY C N
Sbjct: 279 PHIQWLKHIVNGSSFGADGFPYVQVLKTADINSSEVEVLYLRNVSAEDAGEYTCLAGNS 338

Query: 254 IGEANQSAWLTVTRPVAKALEERPAMVTSPLYLEIIIIYCTGAPLISCMGLGSVIIYKMKSG 313
IG + QSAWLTV P P + C + + ++SG
Sbjct: 339 IGLSYQSAWLTVL-----PGTGRIP-----HLTCDSLTPAGRTKSPTLQFSLESG 383

Query: 314 TKKSDPHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSE 373
+ + E LS LVSCAYQVARGM+YL S+KCIHRDLAARNVLVTEDNMVKIADF
Sbjct: 384 S-----SGKSSSS-----LVRGVRLSSSGPALLAGLVLS 411

Query: 374 YELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAAEIGLDDKDKPNRVTKVAVKMLKSDATE 433
+LP DP WE PRDRLVLGKPLGEGCFGQV AEA G+D +P++ + VAVKMLK +A++
Sbjct: 412 LDLPDLPLWEFPRDRLVLGKPLGEGCFGQVRAEAFGMDPARPDQASTVAVKMLKDNASD 471

Query: 434 KDLSDLISEMEMMKMIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLE 493
KDL+DL+SEME+MK+IG+HKNIINLL CTQ+GPLYVIVE A+KGNLRE+L+ARRPPG +
Sbjct: 472 KDLADLVSEMEVMKLGIRHKNIINLLGVCTQEGPLYVIVECAAKGNLREFLRARRPPGPD 531

Query: 494 YCYNPSHNPEEQLSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNMVKIADF 553
+ + E LS LVSCAYQVARGM+YL S+KCIHRDLAARNVLVTEDNMVKIADF
Sbjct: 532 LSPDGPSSSEGFLSFPVLVSCAYQVARGMQYLESRKCIHRDLAARNVLVTEDNMVKIADF 591

Query: 554 GLARDIHHIDYKKTTNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYP 613
GLAR +HHIDYKKTTNGRLPVKWMAPALFDR+YTHQSDVWSFG+LLWEIFTLGGSPYP
Sbjct: 592 GLARGVHHIDYKKTSNGRLPVKWMAPALFDRVYTHQSDVWSFGILLWEIFTLGGSPYP 651

Query: 614 GVPVEELFKLLKEGHRMDKPSNCTNELYMMRDCWHAVPSQRPTFKQLVEVLDRIVALT 673
G+PVEELF LL+EGHRMD+P +C ELY +MR+CWHA PSQRPTFKQLVE LD+++ L
Sbjct: 652 GIPVEELFSLREGHRMDRPPHCPPELYGLMRECWAAPPSQRPTFKQLVEALDKVL-LAV 710

Query: 674 NQEYLDLSIPLDQYSPSPFDTRSSTCSSGSDSVFSHEPLP 713
++EYLDL + YSPS D SSTCSS DSVFSH+PLP
Sbjct: 711 SEEYLDLRLTFGPYSPSGGDA-SSTCSS-SDSVFSHDPLP 748

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tr Q8IXC7 Isoform of FGFR2 [FGFR2 AT-I] [Homo sapiens (Human)] 709 AA
Q8IXC7_HUMAN align

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Score = 770 bits (1989), Expect = 0.0  
Identities = 420/753 (55%), Positives = 502/753 (66%), Gaps = 83/753 (11%)

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Query: 1 MWGKWCILFWAVLVATLCTARPAITLPEQDALPSSSEDDDDSSSEKETDNTKPNPV 60
M W + V+ ATL ARP+ +L E L E P
Sbjct: 1 MVSWGRFICLVVVMTATLSLARPSFSLVEDTLEPE-----PP 39

Query: 61 APYWTSPKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHR---IGGYKV 117
Y S + +++ ++++ +C + W K+G P++R IG Y
Sbjct: 40 TKYQIS---QPEYVVAAPGESLEVRCLLKDA--VISWTKDGVHLGPNNRTVLIGY-- 91

Query: 118 RYATWSIIMDSVVPSSDKGNVTCIVENEYGSINHTYQLDVVE----- 158
+ + P D G Y C S + ++V +
Sbjct: 92 -----LQIKGATPRDSGLYACTASRTVDSETWYFMVNVTDAISSGDEDDTDGAEDFVS 145

Query: 159 -----RSPHRPILQAGLPANKTVALGNSVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPD 212
R+P+ + V + V+F C +P P ++WLK NG + +
Sbjct: 146 ENSNNKRAPYWTNTEKMEKRLHAVPAANTVKFRCPAGGNPMPMTMRWLK---NGKEFKQE 201

Query: 213 NLPYVQILKHSNGINSSDAE-VLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVAK 271
+ + G + L + +V + G Y C V N G N + L V P
Sbjct: 202 H-----RIGGYKVRNQHWSLIMESVVPSSDKGNVTCIVENEYGSINHTYHLDVVAP--- 251

Query: 272 ALEERPAMVTSPLYLEIIIIYCTGAPLISCMGLGSVIIYKMKSGTKKSDPHSQMAVHKLAKS 331
+ SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DP SQ AVHKL K
Sbjct: 252 --GREKEITASPDYLEIAIYCIGVFLIACMVVTIILCRMKNTTKKPDPSSQPAVHKLTKR 309

Query: 332 IPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPRDRL 389
IPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+L
Sbjct: 310 IPLRRQVTVSAESSSSSMNSNTPLVRITTRLSSADTPMLAGVSEYELPEDPKWEFFPRDKL 369

Query: 390 VLKPLGEGCFGQVVLAAEIGLDDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMI 449
LGKPLGEGCFGQVVAE+G+DKDKP VAVKMLK DATEKDLSDL+SEMEMMKMI
Sbjct: 370 TLGKPLGEGCFGQVVMMAEAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMMKMI 429

Query: 450 GKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQLSK 509
GKHKNIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++ K
Sbjct: 430 GKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLARRPPGMEYSYDINRVPEEQMTFK 489

Query: 510 DLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNMVKIADFGGLARDIHHIDYKKTT 569
DLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NMVKIADFGGLARDI++IDYKKTT
Sbjct: 490 DLVSTYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFGGLARDINNIDYKKTT 549

Query: 570 NGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPVEELFKLLKEGHR 629
NGRLPVKWMAPALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPG+PVEELFKLLKEGHR

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Sbjct: 550 NGRLPVKWMAPEALFDRVYTHQSDVWSFGVLMWEIPTLGGSPYPGIPVEELFKLLKEGHR 609

Query: 630 MDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQYSP 689  
MDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+EYLDLS PL+QYSP

Sbjct: 610 MDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTNEEYLDLSQPLEQYSP 669

Query: 690 SFPDTRSSSTCSSGSDSVFSHEPLPEEPCLPRHP 722  
S+PDTRSS CSSG+DSVFS +P+P EPCLP++P

Sbjct: 670 SYPDTRSS-CSSGSDSVFSPDPMPYEPCLPQYP 701

tr Q96KE5 Fibroblast growth factor receptor 4 variant [Homo sapiens (Human)] 592 AA  
Q96KE5\_HUMAN align

Score = 735 bits (1898), Expect = 0.0  
Identities = 377/593 (63%), Positives = 452/593 (76%), Gaps = 20/593 (3%)

Query: 126 MDSVVPSPDKGNYTCIVENEYGSINHTYQLDVVERSHPHPIQAGLPANKTVALGNSNVEFM 185  
M+SVVPSD+G YTC+VEN GSI + Y LDV+ERSPHRPILQAGLPAN T +GS+VE +

Sbjct: 1 MESVVPSPDRGTYTCLVENAVGSIRYNYLLDLVLESPHPIQAGLPANTTAVVGSDEVLL 60

Query: 186 CKVYSDQPHIQWLKHIEVNGSKIGPDNLPYVQILKHSGINSDDAEVLTFLNVTEAQSSE 245  
CKVYSD QPHIQWLKHI +NGS G D PYVQ+LK + INSS+ EVL L NV+ +GE

Sbjct: 61 CKVYSDAQPHIQWLKHIVINGSSFGADGFPYVQVLKTADINSSEVEVLYLRNVSAEDAGE 120

Query: 246 YVCKVSNYIGEANQSAWLTVTRPVAKALEERP---AVMTSPLYLEIIYCTGAFLISCM 302  
Y C N IG + QSAWLTV EE P A Y +II+Y +G+ ++ +L

Sbjct: 121 YTCLAGNISGLSYQSAWLTVP-----EEDPTWTAAPEARYTDIILYASGSLALAVLL 174

Query: 303 GSVIIYKMKSGTKKSDFHSQ--MAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRL 360  
++ ++ G H + V KL++ PL RQ ++ + SS +S LVR RL

Sbjct: 175 ---LLARLYRQCALHGRHPRPATVQKLSR-FPLARQFSLGSSGSKSSSS--LVRGVRL 228

Query: 361 SSSGTPLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAGLDKDKPNRVT 420  
SSSG +LAG+ +LP DP WE PRDRLVLGKPLGEGCFGQVV AEA G+D +P++ +

Sbjct: 229 SSSGPALLAGLVSLDPLDPLWEFPRDRLVLGKPLGEGCFGQVVRARAFGMDPARPDQAS 288

Query: 421 KVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIINLLEACTQDGPLYVIVEYASKGNL 480  
VAVKMLK +A++KDL+DL+SEME+MK+IG+HKNIINLL CTQ+GPLYVIVE A+KGNL

Sbjct: 289 TVAVKMLKDNASDKDLADLVSEMEVMKLIGRHKNIINLLGVCTQEGPLYVIVECAAKGNL 348

Query: 481 REYLQARRPPGLECYNPSHNPFEELSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNV 540  
RE+L+ARRPPG + + + E LS LVSCAYQVARGM+YL S+KCIHRDLAARNV

Sbjct: 349 REFLRARPPGPDLSPDGPRSSGFLSFPVLVSCAYQVARGMQYLESRCKIHRDLAARNV 408

Query: 541 LVTEDNMVKIADFLGARDIHHIDYKKTNGRLPVKWMAPEALFDRIYTHQSDVWSFGVL 600  
LVTEDNMVKIADFLGAR +HHIDYKKT+NGRLPVKWMAPEALFDR+YTHQSDVWSFG+L

Sbjct: 409 LVTEDNMVKIADFLARGVHHIDYKKTNGRLPVKWMAPEALFDRVYTHQSDVWSFGIL 468

Query: 601 LWEIFTLGGSPYPGPVPEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQ 660  
LWEIFTLGGSPYPG+PVEELF LL+EGHRMD+P +C ELY +MR+CWHA PSQRPTFKQ

Sbjct: 469 LWEIFTLGGSPYPGIPVEELFSLLEGHHRMDRPPHCPPELYGLMRECWAAPSQRPTFKQ 528

Query: 661 LVEVLDRIVALTSNQEYLDLSIPLDQYSPSFPDTRSSSTCSSGSDSVFSHEPLP 713  
LVE LD+++ L ++EYLDL + YSPS D SSTCSS DSVFSH+PLP

Sbjct: 529 LVEALDKVL-LAVSEEYLDLRLTFGPYSPSGGDA-SSTCSS-SDSVFSHDPLP 578

sp\_vs P21802-15 Isoform 15 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 705 AA  
FGFR2\_HUMAN (Human)] align

Score = 685 bits (1768), Expect = 0.0  
Identities = 390/758 (51%), Positives = 480/758 (63%), Gaps = 97/758 (12%)

Query: 1 MWGWKCLFWAVLVATLCTARFAPTLPEQDALPSSDDDDDDSSSEKETDNTKPNPV 60  
M W + V+ ATL ARP+ +L E L E P

Sbjct: 1 MVSWGRFICLVVVVMTATLSLARPSFSLVEDTTLEPEE-----PP 39

Query: 61 APYWTSPKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHR---IGGYKV 117  
Y S + +++ +++++ +C + W K+G P++R IG Y

Sbjct: 40 TKQKIS---QPEVYVAAPGESLEVRCLLKDA--VISWTKDGVHLGPNNRTVLIGEY-- 91

Query: 118 RYATWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQLDVVE----- 158  
+ + P D G Y C S + ++V +

Sbjct: 92 -----LQIKGATPRDSGLYACTASRTVDSETWYFMVNVTDAISSGDEDDTDGAEDFVS 145

Query: 159 -----RSPHPIQAGLPANKTVALGNSNVEFMCKVYSDQPHIQWLKHIEVNGSKIGPD 212  
R+P+ + V + V+F C +P P ++WLK NG + +

Sbjct: 146 ENSNNKRAPYWTNTEKMEKRLHAVPAANTVKFRCPAGGNPMTMRWLK----NGKEFKQE 201

Query: 213 NLPYVQILKHSGINSDDAE-VLTFLNVTEAQSGEYVCKVSNYIGEANQSAWLTVT----- 266

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      +      + G      +      L + +V + G Y C V N G N + L V
Sbjct: 202 H-----RIGGYKVRNQHWSLIMESVVPSPDKGNYTCVVENEYGSINHTYHLDVVERSPH 254
Query: 267 RPKAKALEERPAVMTSPPLYLEIIYCTGAFLISCMGLGSVIIYKMKSGTKKSDFHSQMAVH 326
      RP+ +A      PA ++ + ++      C + +      I +      K+G+K
Sbjct: 255 RPILQA--GLPANASTVVGDDVEFVCK-VYSDAQPHIQWIKHVEKNGSKYGP----- 303
Query: 327 KLAKSIPLRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWEL 384
      +P + + VSA+SS+SMNS      LVR +RLSS+      TPMLAGVSEYELPEDP+WE
Sbjct: 304 ---DGLPYLKVLVKVAESSSSMNSNTPLVRIITRLSSTADTPMLAGVSEYELPEDPKWEF 360
Query: 385 PRDRLVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEME 444
      PRD+L LGKPLGEGCFGQVV+AEA+G+DKDKP      VAVKMLK DATEKDLSDL+SEME
Sbjct: 361 PRDKLTLLGKPLGEGCFGQVMAEAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEME 420
Query: 445 MMKMIGKHKNI INLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEE 504
      MMKMIGKHKNI INLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEE
Sbjct: 421 MMKMIGKHKNI INLLGACTQDGPLYVIVEYASKGNLREYLRRARRPPGMEYSYDINRVPEE 480
Query: 505 QLSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGGLARDIHHIDY 564
      Q++ KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NVMKIADFGGLARDI++IDY
Sbjct: 481 QMTPKDLVSCITYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFGGLARDINNIDY 540
Query: 565 YKKTNGRLPVKWMAPALFDRITYTHQSDVWSFGVLLWEIFTLGGSPYPGVPVEELFKLL 624
      YKKTNGRLPVKWMAPALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPG+PVEELFKLL
Sbjct: 541 YKKTNGRLPVKWMAPALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLL 600
Query: 625 KEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPL 684
      KEGHRMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+EYLDLS PL
Sbjct: 601 KEGHRMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTNEEYLDLSQPL 660
Query: 685 DQYSPSPDTRSSSCSSGEDSVFSHEPLPEEPCLPHP 722
      +QYSPS+PDTRSS CSSG+DSVFS +P+P EPCLP++P
Sbjct: 661 EQYSPSPDTRSS-CSSGDDSVFSPDPMPYEPCLPQYP 697

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tr Q59FL9      Fibroblast growth factor receptor 3 isoform 1 variant (Fragment) 879 AA
Q59FL9_HUMAN  [Homo sapiens (Human)] align

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Score = 684 bits (1764), Expect = 0.0  
 Identities = 346/539 (64%), Positives = 421/539 (78%), Gaps = 15/539 (2%)

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Query: 34 PSSDDDDDDSSSEKETDNTKPNFVAPYWTSPKMEKKLHAVPAAKTVKFKCPSSGTP 93
      PSS DD+D +D      E ++T + APYWT PE+M+KKL AVPA TV+F+CP++G P
Sbjct: 216 PSSDDDDGED-----EAEDTGVDTGAPYWTRPERMDKLLAVPAANTVRFRCPAAGNP 269
Query: 94 NPTLRWLKNGKEBPKPDHRIGGYKVRYATWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQ 153
      P++ WLKNG+EF+ +HRIGG K+R+ WS++M+SVVPSD+GNYTC+VEN++GSI TY
Sbjct: 270 TPSIWLKNGREFRFGHRIGGIKLRHQQVSLVMESVVPSPDRGNYTCVENKFGSIRQTYT 329
Query: 154 LDVVERSHPRPILQAGLPANKTVALGSNVEFMCKVYSDQPQPHIQWLKHIEVNGSKIGPDN 213
      LDV+ERSHPRPILQAGLPAN+T LGS+VEF CKVYSD QPHIQWLKH+EVNGSK+GPD
Sbjct: 330 LDVLSERSHPRPILQAGLPANQTAVLGSDFVHFCKVYSDAQPHIQWLKHIEVNGSKVGPDPG 389
Query: 214 LPYVQILKHSGINSDDAE--VLTLPNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVAK 271
      PYV +LK +G N++D E VL+L NVT +GEY C N IG ++ SAWL V P +
Sbjct: 390 TPYVTVLKTAGANTTDKELEVLSLHNVTEDAGEYTCLAGNSIGFHHSAWLVVL-PAEE 448
Query: 272 ALERPAVMTSPPLYLEIIYCTGAFLISCMGLGSVIIYKMKSGTKKSDFHSQMAVHLAKS 331
      L E A      +Y I+ Y G FL ++ +V + ++S KK      VHK+++
Sbjct: 449 ELVE--ADEAGSVYAGILSYGVGFFLFILVVAAVTLCLRLSPPKG--LGSPTVHKISR- 503
Query: 332 IPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVL 391
      PL+RQ VS +S+ASM+S      LVR +RLSS P LA VSE ELP DP+WEL R RL L
Sbjct: 504 FPLKRQ-QVSLASNAMSNTPLVRIARLSSGEGPTLANVSELELPADPKWELSRARLTL 562
Query: 392 GKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGK 451
      GKPLGEGCFGQVV+AEAIG+DKD+ +      VAVKMLK DAT+KDLSDL+SEMEMMKMIGK
Sbjct: 563 GKPLGEGCFGQVMAEAGIDKDRAAKPVTVAVKMLKDDATDKDLSDLVSEMEMMKMIGK 622
Query: 452 HKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQLSKDL 511
      HKNIINLL ACTQ GPLYV+VEYA+KGNLRE+L+ARRPPGL+Y ++ PEEQL+ KDL
Sbjct: 623 HKNIINLLGACTQGGPLYVLVEYAAKGNLREFLRARRPPGLDYSDFTCKPPEEQLTFFKDL 682
Query: 512 VSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGGLARDIHHIDYKKTN 570
      VSCAYQVARGMEYLAS+KCIHRDLAARNVLVTEDNVMKIADFGGLARD+H++DYKKTN
Sbjct: 683 VSCAYQVARGMEYLASQKCIHRDLAARNVLVTEDNVMKIADFGGLARDVHNLDYKKTN 741

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tr A8E633      Putative uncharacterized protein (Fragment) [Homo sapiens (Human)] 480 AA
A8E633_HUMAN align

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Score = 646 bits (1667), Expect = 0.0  
 Identities = 328/474 (69%), Positives = 383/474 (80%), Gaps = 9/474 (1%)

Query: 243 SGEYVCKVSNYIGEANQSAWLTVTTRPVAKALEERPAVMTSPLYLEIIIIYCTGAFILSCML 302  
 +GEY C N IG ++ SAWL V P + L E A +Y I+ Y G FL ++  
 Sbjct: 8 AGEYTCAGNSIGFSSHSWLVVL-PAEEELVE--ADEAGSVYAGILSYGVGFLLFILVV 64

Query: 303 GSVIIYKMKSGTKKSDPHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSS 362  
 +V + +++S KK VHK+++ PL+RQV S +S+ASM+S LVR +RLSS  
 Sbjct: 65 AAVTLCRLRSPPKKG--LGSPTVHKISR-FPLKRQV--SLESNASMSSNTPLVRIARLSS 119

Query: 363 SGTPLMAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKV 422  
 P LA VSE ELP DP+WEL R RL LGKPLGEGCFGQVV+AEAIG+DKD+ + V  
 Sbjct: 120 GEGPTLANVSELELPADPKWELSRARLTGKPLGEGCFGQVVMAEAIKIDKRAAKPVTV 179

Query: 423 AVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIINLLEACTQDGPVYVIVEYASKGNLRE 482  
 AVKMLK DAT+KDLSDL+SEMEMMKMIGKHKNIINLL ACTQ GPLYV+VEYA+KGNLRE  
 Sbjct: 180 AVKMLKDDATDKDLSDLVSEMEMMKMIGKHKNIINLLGACTQGGPLYVVLVEYAAKGNLRE 239

Query: 483 YLQARRPPGLECYNPSHNPEQLSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLV 542  
 +L+ARRPPGL+Y ++ PEEQL+ KDLVSCAYQVARGMEYLAS+KCIHRDLAARNVLV  
 Sbjct: 240 FLRARRPPGLDYSPDTCKPPEQLTFKDLVSCAYQVARGMEYLASQKCIHRDLAARNVLV 299

Query: 543 TEDNVMKIADFGLARDIHHIDYKKTNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLW 602  
 TEDNVMKIADFGLARD+H++DYKKTNGRLPVKWMAPALFDR+YTHQSDVWSFGVLLW  
 Sbjct: 300 TEDNVMKIADFGLARDVHNLDDYKKTNGRLPVKWMAPALFDRVYTHQSDVWSFGVLLW 359

Query: 603 EIPTLGGSPYPGVPEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLV 662  
 EIPTLGGSPYPG+PVEELFKLLKEGHRMDKP+NCT++LYM+MR+CWAH PSQRPTFKQLV  
 Sbjct: 360 EIPTLGGSPYPGIPVEELFKLLKEGHRMDKPANCTHDLYMIMRECWAHAPSQRPTFKQLV 419

Query: 663 EVLDRIVALTSNQEYLDLSIPLDQYSPSPFDTRSSSTCSSGEDSVFSHEPLPEEP 716  
 E LDR++ +TS EYLDLS P +QYSP DT SS+ SSG+DSVF+H+ LP P  
 Sbjct: 420 EDLDRVLTVTSTDEYLDLSAPFEQYSPGGQDTPSSS--SSGDDSVFAHDLLEPPAP 472

tr Q0IJ44 FGFR3 protein (Fragment) [FGFR3] [Homo sapiens (Human)] 480 AA  
 Q0IJ44\_HUMAN align

Score = 646 bits (1666), Expect = 0.0  
 Identities = 328/474 (69%), Positives = 383/474 (80%), Gaps = 9/474 (1%)

Query: 243 SGEYVCKVSNYIGEANQSAWLTVTTRPVAKALEERPAVMTSPLYLEIIIIYCTGAFILSCML 302  
 +GEY C N IG ++ SAWL V P + L E A +Y I+ Y G FL ++  
 Sbjct: 8 AGEYTCAGNSIGFSSHSWLVVL-PAEEELVE--ADEAGSVYAGILSYGVGFLLFILVV 64

Query: 303 GSVIIYKMKSGTKKSDPHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSS 362  
 +V + +++S KK VHK+++ PL+RQV S +S+ASM+S LVR +RLSS  
 Sbjct: 65 AAVTLCRLRSPPKKG--LGSPTVHKISR-FPLKRQV--SLESNASMSSNTPLVRIARLSS 119

Query: 363 SGTPLMAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKV 422  
 P LA VSE ELP DP+WEL R RL LGKPLGEGCFGQVV+AEAIG+DKD+ + V  
 Sbjct: 120 GEGPTLANVSELELPADPKWELSRARLTGKPLGEGCFGQVVMAEAIKIDKRAAKPVTV 179

Query: 423 AVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIINLLEACTQDGPVYVIVEYASKGNLRE 482  
 AVKMLK DAT+KDLSDL+SEMEMMKMIGKHKNIINLL ACTQ GPLYV+VEYA+KGNLRE  
 Sbjct: 180 AVKMLKDDATDKDLSDLVSEMEMMKMIGKHKNIINLLGACTQGGPLYVVLVEYAAKGNLRE 239

Query: 483 YLQARRPPGLECYNPSHNPEQLSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLV 542  
 +L+ARRPPGL+Y ++ PEEQL+ KDLVSCAYQVARGMEYLAS+KCIHRDLAARNVLV  
 Sbjct: 240 FLRARRPPGLDYSPDTCKPPEQLTFKDLVSCAYQVARGMEYLASQKCIHRDLAARNVLV 299

Query: 543 TEDNVMKIADFGLARDIHHIDYKKTNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLW 602  
 TEDNVMKIADFGLARD+H++DYKKTNGRLPVKWMAPALFDR+YTHQSDVWSFGVLLW  
 Sbjct: 300 TEDNVMKIADFGLARDVHNLDDYKKTNGRLPVKWMAPALFDRVYTHQSDVWSFGVLLW 359

Query: 603 EIPTLGGSPYPGVPEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLV 662  
 EIPTLGGSPYPG+PVEELFKLLKEGHRMDKP+NCT++LYM+MR+CWAH PSQRPTFKQLV  
 Sbjct: 360 EIPTLGGSPYPGIPVEELFKLLKEGHRMDKPANCTHDLYMIMRECWAHAPSQRPTFKQLV 419

Query: 663 EVLDRIVALTSNQEYLDLSIPLDQYSPSPFDTRSSSTCSSGEDSVFSHEPLPEEP 716  
 E LDR++ +TS EYLDLS P +QYSP DT SS+ SSG+DSVF+H+ LP P  
 Sbjct: 420 EDLDRVLTVTSTDEYLDLSAPFEQYSPGGQDTPSSS--SSGDDSVFAHDLLEPPAP 472

sp\_vs P22607-3 Isoform 3 of P22607 - Homo sapiens (Human) [FGFR3] [Homo sapiens 694 AA  
 FGFR3\_HUMAN (Human)] align

Score = 625 bits (1611), Expect = e-178  
 Identities = 332/547 (60%), Positives = 393/547 (71%), Gaps = 32/547 (5%)

Query: 176 VALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKHSNGINSSDAEVLTL 235  
 V + V F C + P P I WLK NG + ++ L+H + L +  
 Sbjct: 166 VPAANTVRFRCPAAGNPTPSISWLK---NGREFRGEHRIGGIKLRHQQWS-----LVM 215

Query: 236 FNVTEAQSGEYVCKVSNYIGEANQSAWLTVT----RPVAKALEERPAVMTSPLYLEIII 290  
 +V + G Y C V N G Q+ L V RP+ +A PA T+ L ++  
 Sbjct: 216 ESVPSPDRGNYTCVVENKFGSIRQTYTLDVLESPHRPILQA--GLPANQTAVLGSDVEF 273

Query: 291 YCTGAFILISCMGVSIIYKMKSGTKKSDFHSMQMAVHKLAKE-IPLRRQVTVSADSSASMN 349  
 +C +Y + H ++ K+ P + VS +S+ASM+  
 Sbjct: 274 HCK-----VYSDAQPHIQWLKHVEVNGSKVGPDPGTPYVTVLKVSLASNAMS 320

Query: 350 SGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAI 409  
 S LVR +RLSS P LA VSE ELP DP+WEL R RL LGKPLGEGCFGQVVAEAI  
 Sbjct: 321 SNTPLVRIARLSSSGGPTLANVSELELPADPKWELSRARLTGKPLGEGCFGQVVMAEAI 380

Query: 410 GLDKDKPNRVTKVAVKMLKSDATEKDLSLISEMEMMKMIGKHKNIIINLLEACTQDGPLY 469  
 G+DKD+ + VAVKMLK DAT+KDLSL+SEMEMMKMIGKHKNIIINLL ACTQ GPLY  
 Sbjct: 381 GIDKDRAAKFPVTAVKMLKDDATDKDLSLISEMEMMKMIGKHKNIIINLLGACTQGGPLY 440

Query: 470 VIVEYASKGNLREYLQARRPPGLECYNPSHNPPEEQLSKDLVSCAYQVARGMEYLASKK 529  
 V+VEYA+KGNLRE+L+ARRPPGL+Y ++ PEEQL+ KDLVSCAYQVARGMEYLAS+K  
 Sbjct: 441 VLVEYAAKGNLREPLRARPPGLDYSDFTCKPPEEQLTFLDLVSCAYQVARGMEYLASQK 500

Query: 530 CIHRDLAARNVLVTEDNMVKIADFGGLARDIHHIDYKKTNGRLPVKWMAPALFDRIYT 589  
 CIHRDLAARNVLVTEDNMVKIADFGGLARD+H++DYKKTNGRLPVKWMAPALFDR+YT  
 Sbjct: 501 CIHRDLAARNVLVTEDNMVKIADFGGLARDVHNLDDYKKTNGRLPVKWMAPALFDRVYT 560

Query: 590 HQSDVWSFGVLLWEIFTLGGSPYPGPVPEELFKLLKEGHRMDKPSNCTNELYMMMRDCWH 649  
 HQSDVWSFGVLLWEIFTLGGSPYPGP+PVEELFKLLKEGHRMDKPNCT++LYM+MR+CWH  
 Sbjct: 561 HQSDVWSFGVLLWEIFTLGGSPYPGPVPEELFKLLKEGHRMDKPNCTHDLYMIMRECWH 620

Query: 650 AVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQYSPSPDPTRSSSTCSSGDSVFSH 709  
 A PSQRPTFKQLVE LDR++ +TS EYLDLS P +QYSP DT SS+ SSG+DSVF+H  
 Sbjct: 621 AAPSQRPTFKQLVEDLDRVLTVTSTDEYLDLSAPFQYSPGGQDTPSSS--SSGDSVFAH 679

Query: 710 EPLPEEP 716  
 + LP P  
 Sbjct: 680 DLLPPAP 686

Score = 280 bits (717), Expect = 5e-75  
 Identities = 131/213 (61%), Positives = 165/213 (77%), Gaps = 7/213 (3%)

Query: 34 PSEDDDDDDSSSEKETDNTKPNPVAPYWTSPKMEKKLHAVPAAKTVKPKCPSSGTP 93  
 PSS DD+D +D E ++T + APYWT PE+M+KKL AVPA TV+F+CP++G P  
 Sbjct: 129 PSSDDEDEDG-----EAEDTGVDTGAPYWTRPERMDKKLLAVPAANTVFRCPAAGNP 182

Query: 94 NPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPDKGNYTCIVENEYGSINHTYQ 153  
 P++ WLKNG+EF+ +HRIGG K+R+ WS++M+SVVPSD+GNYTC+VEN++GSI TY  
 Sbjct: 183 TPSISWLKNGREFRGEHRIGGIKLRHQQWSLVMSVVPSPDRGNYTCVVENKFGSIRQTYT 242

Query: 154 LDVVERSPhRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDN 213  
 LDV+ERSPhRPILQAGLPAN+T LGS+VEF CKVYSD QPHIQWLKH+EVNGSK+GPD  
 Sbjct: 243 LDVLESPHRRPILQAGLPANQTAVLGSDVEFHCKVYSDAQPHIQWLKHVEVNGSKVGPDG 302

Query: 214 LPYVQILKHS-GINSSDAEVLTLFNVTEAQSGE 245  
 PYV +LK S N+S + L + SGE  
 Sbjct: 303 TPYVTVLKVSLASNASSNTPLVRIARLSSGE 335

tr Q59F30 Fibroblast growth factor receptor 4 variant (Fragment) [Homo sapiens 1034 AA  
 Q59F30\_HUMAN (Human)] align

Score = 553 bits (1426), Expect = e-157  
 Identities = 285/450 (63%), Positives = 348/450 (77%), Gaps = 13/450 (2%)

Query: 268 PVAKALEERPAVMTSP--LYLEIIIIYCTGAPLISCMGVSIIYKMKSGTKKSDFHSSQ--M 323  
 P A+A E+ +P Y +II+Y +G+ ++ +L ++ ++ G H +  
 Sbjct: 580 PCARABEDPTWTAAPAEARYTDIILYAGSGLALAVLL---LLARLYRGQALHGRHPRPPA 636

Query: 324 AVHKLAKSIPLRRQVTVSADSSASMN SGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWE 383  
 V KL++ PL RQ ++ + SS +S LVR RLSSSG +LAG+ +LP DP WE  
 Sbjct: 637 TVQKLSR-FPLARQFSLESGSSGKSSS--LVRGVRLSSSGPALLAGLVSLDLPLDPLWE 693

Query: 384 LPRDRLVLGKPLGEGCFGQVVLAEAIIGLDKDKPNRVTKVAVKMLKSDATEKDLSLISEM 443  
 PRDRLVLGKPLGEGCFGQVV AEA G+D +P++ + VAVKMLK +A++KDL+DL+SEM  
 Sbjct: 694 FPRDRLVLGKPLGEGCFGQVVAEAFGMDPARPDQASTVAVKMLKDNASDKDLADLVSEM 753

Query: 444 EMMKMIGKHKNIIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNP 503  
 E+MK+IG+HKNIINLL CTQ+GPLYVIVE A+KGNLRE+L+ARRPPG + + + E

Sbjct: 754 EVMKLIQRHNIINLLGVCTQEGPLYVIVECAAKGNLREFLRARRPPGPDLSPDGPRSS 813

Query: 504 EQLSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGIARDIHIIID 563  
 LS LVSCAYQVARGM+YL S+KCIHRDLAARNVLVTEDNVMKIADFGIAR +HHID

Sbjct: 814 GPLSPFVLVSCAYQVARGMQYLESRKCIHRDLAARNVLVTEDNVMKIADFGIARGVHHID 873

Query: 564 YYKKTNGRLPVLKWMAPALFDRITYTHQSDVWSFGVLLWEIFTLGGSPYPGVPVEELFKL 623  
 YYKKT+NGRLPVLKWMAPALFDR+YTHQSDVWSFG+LLWEIFTLGGSPYPG+PVEELF L

Sbjct: 874 YYKKTNGRLPVLKWMAPALFDRVYTHQSDVWSFGILLWEIFTLGGSPYPGIPVEELFSL 933

Query: 624 LKEGHRMDKPSNCTNELYMMRDWCWHA VPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIP 683  
 L+EGHRMD+P +C ELY +MR+CWHA PSQRPTFKQLVE LD+++ L ++EYLDL +

Sbjct: 934 LREGHRMDRPPHCPPELYGLMRECWHAAAPSQRPTFKQLVEALDKVL-LAVSEEYLDLRLT 992

Query: 684 LDQYSPSPDTRSSSTCSSGSDSVFSHEPLP 713  
 YSPS D SSTCSS DSVFSH+PLP

Sbjct: 993 FGPYSPSGDA-SSTCSS-SDSVFSHDPLP 1020

Score = 295 bits (754), Expect = 2e-79  
 Identities = 134/209 (64%), Positives = 164/209 (78%)

Query: 57 PNPVAPYWTSPKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYK 116  
 P P APYWT P++MEKKLHAVPA TVKF+CP++G P PT+RWLK+G+ F ++RIGG +

Sbjct: 257 PCPPAPYWTHPQRMEKKLHAVPAGNTVKFRCPAAGNPTPTIRWLKDGQAFHGENRIGGIR 316

Query: 117 VRYATWSIIIMDSVPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTV 176  
 +R+ WS++M+SVVPSD+G YTC+VEN GSI + Y LDV+ERSPHRPILQAGLPAN T

Sbjct: 317 LRHQHWSLVMSVSPSDRGTYTCLVENAVGSIIRYNYLLDVLESPHRPILQAGLPANTTA 376

Query: 177 ALGSNVEFMCKVYSDFPHIQWLKHIEVNGSKIGPDNLPYVQILKHSGINSSDAEVLTLF 236  
 +GS+VE +CKVYSD QPHIQWLKHI +NGS G D PYVQ+LK + INSS+ EVL L

Sbjct: 377 VVGSDEVLLCKVYSDAQPHIQWLKHIVINGSSFGADGFFVQVLKTADINSSEVEVLYLR 436

Query: 237 NVTEAQSGEYVCKVSNYIGEANQSAWLTV 265  
 NV+ +GEY C N IG + QSAWLTV

Sbjct: 437 NVSAEDAGEYTCLAGNSIGLSYQSAWLTV 465

Subset of the database(s) listed below  
 Number of letters searched: 35,064,127  
 Number of sequences searched: 82,088

Database: UniProtKB Homo sapiens  
 Posted date: Nov 12, 2007 6:33 PM  
 Number of letters in database: 25,263,043  
 Number of sequences in database: 64,426

Database: UniProtKB\_HUMAN.01  
 Posted date: Nov 12, 2007 6:36 PM  
 Number of letters in database: 9,801,084  
 Number of sequences in database: 17,662

Lambda	K	H
0.316	0.133	0.405

Gapped		
Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62  
 Gap Penalties: Existence: 11, Extension: 1  
 Number of Hits to DB: 59,077,092  
 Number of Sequences: 2526181  
 Number of extensions: 2919052  
 Number of successful extensions: 26662  
 Number of sequences better than 10.0: 1000  
 Number of HSP's better than 10.0 without gapping: 1277  
 Number of HSP's successfully gapped in prelim test: 935  
 Number of HSP's that attempted gapping in prelim test: 15141  
 Number of HSP's gapped (non-prelim): 6214  
 length of query: 733  
 length of database: 35,064,127  
 effective HSP length: 114  
 effective length of query: 619  
 effective length of database: 25,706,095  
 effective search space: 15912072805  
 effective search space used: 15912072805  
 T: 11  
 A: 40  
 X1: 16 ( 7.3 bits)  
 X2: 38 (14.6 bits)  
 X3: 64 (24.7 bits)  
 S1: 41 (21.6 bits)  
 S2: 68 (30.8 bits)  
 Wallclock time: 4 seconds

